

DB 466 GNTTITNTINGTNGCNCNWSNCNCNCNCNCNTNTNGCNTATGNSN 525
DY 341 CAGGACAGGGGACATTATCCAGAGAGATTCTAGAGCTCTATTACATCTGACCTC 400
DB 526 MNGSARTTGGATGATATHTYNGNSGNGGNTTACAGAGANTTTTATATYNGCNTN 585
DY 401 AAGACATGATGGGATAGATAGATGGGTGATCGTTTGTCTCAGGGGGGTTTGTGATC 460
DB 586 AARGANTYNCATYTNKABWNTGGTNTNGCNCNTCYCCNARGCNCATTTATGYN 645
DY 461 AAMACAGACTCAGCATGTCATCTGCTACTGCTGACTGACCTGACTGCTTGAGAA 520
DB 646 AARGNGAGAYGANTTGTGNCATGNCNAGTNGATTTVTKNAGTNGT 705
DY 521 AMAGAMACACAGGTTTTCTAGTGGCTTCGAACTCATAGATTTCCATCAGSNG 580
DB 706 GAYCCNCNCARGAYTNTNGTNGGAYGTNTHTGNCAGCNCNTGNCNATGNAAT 765
DY 581 CANTCAGCAGATGTTTGTCTGATTAATCTGATATCCGFGGAGACAGTACCATC 640
DB 766 ACNAAAGTNAATATTTATGNCNCNWSNATGTATGNSNCNCAATATCCNCAT 825
DY 641 TCTCCGACACGGCTACGCTGTTCTGCGCATGTCGCGCATGAGGTGATATGCTCC 700
DB 826 CGNGSGNGGNGSNTAYGTATGNSGNCNAGTNGNKNNTGNCAGCNATATC 885
DY 701 AAGAGGCTCCGACATTAATCTGAGAGAGCGTGTGCGGGCTTGGCTGAAAGGCTC 760
DB 886 GARGATCGNCARTTNTTNGSNATHGAYGTNTTGTGNGMATGTGTGNGNKNNTN 945
DY 761 AKATCAG 768
DB 946 GONTNMS 953

Search completed: April 11, 2003, 20:07:23
Job time : 176.108 secs

Genome version 5.1.4.p5.4578
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OW nucleic - nucleic search, using sw model

Run on: April 11, 2003, 15:35:54, Search time 1036.47 seconds
14547.424 Million cell updates/sec

Title: score: US-09-914-152-2_COPY_401_L331
Sequence: 1 aatgggttcctccagatga.....gggaagattccgcgtc 931

Scoring table: IDENTIFY_NUC Gap 10.0, Gapex 1.0
1 aatgggttcctccagatga.....gggaagattccgcgtc 931

Searched: 16154056 seqs, 809774376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
match of the same length as the query sequence printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
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C 2	366.6	39.4	434 12 BF748181
C 2	366.6	39.4	BF748181 FC3-BN001
C 3	326	25.1	338 9 AJ003597
C 3	326	25.1	AJ003597 AJ003597
C 4	234	25.1	400 17 A2768940
C 4	234	25.1	A2768940 IM0569K09
C 5	159.2	17.3	636 13 AL330238
C 5	159.2	17.3	AL330238 Tetradodon
C 6	135	14.5	1514 11 BC955084
C 6	135	14.5	BC955084 Mus muscu

7	132.2	14.2	596 13 BC501651
8	126.8	13.8	BC028571 Homo sapi
9	127.3	13.6	BM028571 Homo sapi
10	123.4	13.3	BM028571 Homo sapi
11	123.4	13.3	BM028571 Homo sapi
12	117.2	12.6	965 17 CS045184
13	115.4	12.4	1021 17 CS045184
14	114.8	12.4	1021 17 CS045184
15	114.8	12.4	1021 17 CS045184
16	110.8	11.6	620 9 AL133606
17	107.6	11.6	712 9 AL133606
18	101.4	10.9	966 17 CS045184
19	99.8	10.7	815 10 AL128625
20	99.8	10.7	815 10 AL128625
21	99.8	10.7	815 10 AL128625
22	97.2	10.4	464 9 AA072283
23	97.2	10.4	464 9 AA072283
24	95.4	10.2	411 9 AA072283
25	93.8	10.1	793 12 BG027694
26	93.4	10.0	675 10 BG027694
27	93.4	10.0	675 10 BG027694
28	90.8	9.8	625 13 B0354223
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ALIGNMENTS

BF748181 434 bp mRNA linear EST 10-JAN-2001
FC3-BN001-021000-021-c04 BN0011 Homo sapiens cDNA, mRNA sequence.
BF748181 G1:12074857
EST.
HUMAN
ORGANISM
SOURCES
KEYWORDS
REFERENCES
ADDITIONS
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
(these are the names of the species in the database)
Nassi M.A., da Silva M.A., Bordin S., Costa F.F.,
Goldman G.H., Carvalho A.F., Matukawa A., Bata G.S., Simpson D.H.,
Arinstein A., de Oliveira P.S., Buchner J., Jongeneel V., Ojeda
Simpson A.J., de Souza S.J., de Souza S.J. and
Shotgun sequencing of the human transcriptome with ORF expressed
sequences. Est. Anal. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
200202663
Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil. Tel.: +55-11-3704622
Fax: +55-11-2707001

Seali, sequences@alibio.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/actipr/gethtml.pl?file=RC342-RC3-RN0411-
us-09-914-152-2_copy_401_l331.rst)
Seq primer: pos 18 forward
High quality sequence start: 24
High quality sequence stop: 432

FEATURES

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/db_xref="taxon:9606"
/clone="hnp19-1235"
/note="Organ: breast; normal; Vector: puc18; Site: 1. Small; Insertion: 1. Small; Orientation: 1. Small; Derivation: derived from ORS7ES PCR (U.S. Letters Patent application No. 136,716 - Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of cDNA was performed under low stringency conditions."

BASE COUNT 104 a 117 c 130 g 83 t
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Best Local Similarity 98.94; Pred. No. 5; e-97;
Matches 369; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 559 CATTGAGTTTCCCATCAGCAGCCATCAGCAGAGTGTTCGATGAATTCGATATCC 618
DB 434 CATTGAGTTTCCCATCAGCAGCCATCAGCAGAGTGTTCGATGAATTCGATATCC 375
QY 619 GTGGACAGTACCCAGCATCTCTCTCGGACAGCGTATGTTTCTTGGACAGTGGC 678
DB 374 GTGGACAGTACCCAGCATCTCTCTCGGACAGCGTATGTTTCTTGGACAGTGGC 315
QY 679 GATTCAGGTGTACATGTCTCCAGAGGTCCTCATATTAATTCGAGAGCTGTGTG 738
DB 314 GATTCAGGTGTACATGTCTCCAGAGGTCCTCATATTAATTCGAGAGCTGTGTG 255
QY 739 GGAGCTCTCTCGAAGAGCTGTACATCATATTGAGAGAGCTCCATCCGACAGCTT 798
DB 255 GGAGCTCTCTCGAAGAGCTGTACATCATATTGAGAGAGCTCCATCCGACAGCTT 195
QY 799 TTTCGAGGAGTGTAGCTTCTTCGATAGCTCTTCGAGAGATGTGGCTTCCCATTT 858
DB 194 TTTCGAGGAGTGTAGCTTCTTCGATAGCTCTTCGAGAGATGTGGCTTCCCATTT 135
QY 859 CATCAGAGCTCGAGCTCTTGGACATTCGAGAGCTCTAGAGATTCGCGGGGAGAG 918
DB 134 CATCAGAGCTCGAGCTCTTGGACATTCGAGAGCTCTAGAGATTCGCGGGGAGAG 75
QY 919 TTTCGAGGAGTGTAGCTTCTTCGATAGCTCTTCGAGAGATGTGGCTTCCCATTT 971
DB 75 TTTCGAGGAGTGTAGCTTCTTCGATAGCTCTTCGAGAGATGTGGCTTCCCATTT 62

RESULT 2
LOCUS A201597/338 bp mRNA linear EST 04-DEC-1997
DEFINITION A201597 selected chromosome 21 cDNA library Homo sapiens cDNA
ACCESSION A201597.1 J01278
VERSION A201597.1 GI:2578270
KEYWORDS EST

ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Sulzawsky, I., Runk, E., Nguyen, M., Korn, B., Rohrdanz, B., Lehrach, H., and Vesp, M. L. H.
An integrated transcript map for the whole human chromosome 21

JOURNAL COMMENT

Unpublished (1997).
Contact: Yaspo, M.-L.
Max Planck Institut fuer Molekulare Genetik
Immelstrasse 1, D-10585 Berlin-Fahnen, Germany
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hnp19-1235"
/note="Organ: breast; normal; Vector: puc18; Site: 1. Small; Insertion: 1. Small; Orientation: 1. Small; Derivation: derived from ORS7ES PCR (U.S. Letters Patent application No. 136,716 - Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of cDNA was performed under low stringency conditions."

FEATURES

1..338
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/db_xref="taxon:9606"
/clone="hnp19-1235"
/note="Organ: breast; normal; Vector: puc18; Site: 1. Small; Insertion: 1. Small; Orientation: 1. Small; Derivation: derived from ORS7ES PCR (U.S. Letters Patent application No. 136,716 - Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of cDNA was performed under low stringency conditions."

BASE COUNT 76 a 92 c 82 g 87 t
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Query Match 35.04; Score 326; DB 9; Length 338;
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Matches 329; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 16 CATTGAGTTTCCCATCAGCAGCCATCAGCAGAGTGTTCGATGAATTCGATATCC 75
DB 335 CATTGAGTTTCCCATCAGCAGCCATCAGCAGAGTGTTCGATGAATTCGATATCC 276
QY 776 GTACGATCTAAATCTCTCAAGAGAGCTCTTGTTCAGAGAGAGAGAGAGCTCTCT 135
DB 275 GTACGATCTAAATCTCTCAAGAGAGCTCTTGTTCAGAGAGAGAGAGAGCTCTCT 216
QY 136 TAAGTCCGACAGTACAGCTCGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 195
DB 215 TAAGTCCGACAGTACAGCTCGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 156
QY 195 ATCCACCAAGCTGTGCTGAGCGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 255
DB 155 ATCCACCAAGCTGTGCTGAGCGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 96
QY 256 GTGAGAGAGAGAGCTGTGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 315
DB 95 GTGAGAGAGAGAGCTGTGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 36
QY 315 AACCAAGAGAGAGAGCTGTGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 350
DB 35 AACCAAGAGAGAGAGCTGTGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1

RESULT 3
LOCUS A276840/c
DEFINITION A276840/c mouse 10kb plasmid UOCCIM library Mus musculus genomic
ACCESSION A276840.1 J01288555
VERSION A276840.1 GI:1288555
KEYWORDS GSS

ORGANISM house mouse
Eukaryota; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Sulzawsky, I., Runk, E., Nguyen, M., Korn, B., Rohrdanz, B., Lehrach, H., and Vesp, M. L. H.
An integrated transcript map for the whole human chromosome 21

REFERENCE Sulzawsky, I., Runk, E., Nguyen, M., Korn, B., Rohrdanz, B., Lehrach, H., and Vesp, M. L. H.
An integrated transcript map for the whole human chromosome 21

QY	807	GGGGTAAAGTCTTCGATGCTCTTCAGAGAGATGGTGCCCA	855	QY	563	GAGTTTCGATCGAGAGACCATACGCAAGTGGTTTCGATGAATCTGATATACCGTGG	622
DB	592	ACAGATCACTCGATGGATGATTTGATCTACAGAGCGATATCGACGCCA	640	DB	282	GTGTGGGCATATAGAGATCTGCGGATACATGTCNAGAGATCTGTACCCGAG	341
RESULT 12				DB	623	GAGTGTACCAACCATCTGCTGCGGACCGCTAGCTGTTCTGCGGACGATCGGCAAT	682
CNS05182				DB	342	AGCAATACCGGCGCTTTTGTTCGCGCATGTTAGCTCTTCCTCGGAGATGGCGGAC	401
LOCUS				QY	683	CAGGTGTACATCTCTCCAGAGAGCTCCCATATTAATCTCGAGACAGATCTGTGTGGG	742
DEFINITION				DB	402	CTATTTTATTTACTCTCTTACACACAGGCTGCTGCACCTGGAGAGCGATGATNTGGGT	461
KEYWORDS				QY	743	CTCTGCTCGAGAGCTGACAT	765
SOURCE				DB	462	NTGTGCTTCGCAAGCTGGCAT	484
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REFERENCE				CNS0474/c			
AUTHORS				LOCUS			
JOURNAL				DEFINITION			
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AUTHORS				SOURCE			
TITLE				ORGANISM			
JOURNAL				ACCESSION			
REFERENCE				AL274513			
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High quality sequence stop: 418.

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BASE COUNT

304 a 239 c 238 g 319 t 1 others

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DB 342 GAGTTACTTGGGTGAGAAAGTCTGCTGGGAGATGAGGCTTCACATTTCTTAT 401
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QY 642 GCTCCGAGAGAGGCT 656
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Search completed: April 11, 2003, 22:37:24
Job time: 1046.47 secs

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AUTHORS	Iaktofi, M., Fujimura, A., Taylor, T., Tokoyabe, H., Yada, T., Park, H., S., Toyoda, A., Ishii, K., Tokoyabe, Y., Choi, D.-K., Soeda, E., Polley, A., Mempel, G., Desai, R., Schmitt, J., Schmitt, J., Schmitt, J., Patterson, D., Reichwald, K., Rump, A., Schillabel, M.B., Schudy, A., Zimmermann, S., Rosenthal, A., Kudoh, J., Kawasaka, K., Asakawa, S., Antonarakis, S., Minoshima, S., Shimizu, N., Nordisk, G., Hornischer, K., Brandt, P., Schafro, M., Scheen, O., Desario, A., Reichel, J., Kauer, G., Blocher, H., Kauer, J., Beck, A., Klages, S., Beyer, K., Gardiner, K., Nietz, C., Francis, F., Lehroth, H., Reinhardt, R. and Vaspou, M. Laure.		
TITLE	The DNA sequence of human chromosome 21		
JOURNAL	Nature 356 (1993), 311-319 (1993)		
PMID	20289795		
REFERENCE			
AUTHORS	Rump, A., Degand, E., Hildmann, T., Nordisk, G., Drescher, B., Weber, J., Schattevov, R., Vaspou, M.-L. and Rosenthal, A.		
TITLE	Direct Submission, 1998, Genome Analysis, Institute of Molecular Biotechnology, Buntzenbergstrasse 11, Jena 07745, Germany		
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AUTHORS	Rump, A., Degand, E., Hildmann, T., Nordisk, G., Drescher, B., Weber, J., Schattevov, R., Vaspou, M.-L., Rosenthal, A., Rump, A., Degand, E., Hildmann, T., Nordisk, G., Drescher, B., Weber, J., Schattevov, R., Vaspou, M.-L., Rosenthal, A.		
TITLE	Submitted (05-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Buntzenbergstr. 11, Jena 07745, Germany		
COMMENT	On Feb 7, Location/Qualifiers		

Mon Apr 14 10:18:06 2003

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Page 8

[illegible]

Shizuoka 411-8540, Japan (E-mail:nsaitou@genes.nig.ac.jp, URL: http://sayer.lab.nig.ac.jp/~silver/. Tel: 81-559-81-6790, Fax: 81-559-81-6789)	
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 QY 419 GATGCTGCTGATGCTTTTGGCTCAGGGGGCTTTGTTGATGAAAGAGATCAGAGATG 478
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 QY 479 TCTATCAATGTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 538
 DD 102929 TCTATCAATGTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 102988
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 QY 599 TCTATCAATGTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
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 DD 103169 AACTTGAGAGAGTGTGTTGGGCTCTGCTCGAGAGCTGATGATGATGATGATGATGAT 103228
 QY 779 TCTATCAATGTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 838
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 QY 839 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
 DD 103289 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 103348
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Search completed: April 11, 2003, 20:17:16
 Job time : 2121.98 secs

GenCore version 5.1.4_p54578
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OK nucleic - nucleic search, using sw model

Run on: April 11, 2003, 21:30:39 / Search time 59.5647 seconds
1710.183 Million cell updates/sec

File: us-09-914-152-2_COPY_401_1331

Perfect score: 91
Sequence: 1 aagcattctccgcagatga.....gggaattgctccgcgtgc 931

Scoring table: IDENTITY_WUC

Gapop 10.0 / Gapext 1.0

Searched: 593429 seqs, 43858390 residues 1186858

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0.000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 40 summaries

Database :		Published Applications_NA.*	Query	Score	Match	Length	DB ID	Description
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2	/cgn2_5/pdata2/pubna/ACT_NEM_PUB.seq			2	130.4	14.0	2095	US-09-922-598-208
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4	/cgn2_5/pdata2/pubna/AS06_PUBCOMB.seq			4	130.4	14.0	2095	US-10-063-547-35
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10	/cgn2_5/pdata2/pubna/AS08_PUBCOMB.seq			10	130.4	14.0	2095	US-09-989-734-208
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19	/cgn2_5/pdata2/pubna/AS10_PUBCOMB.seq			19	130.4	14.0	2095	US-10-173-706-161

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best matching printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	130.4	14.0	1773	US-09-739-451-9	Query March
2	130.4	14.0	2095	US-09-922-598-208	Sequence 208, App
3	130.4	14.0	2095	US-09-989-293A-208	Sequence 208, App
4	130.4	14.0	2095	US-10-063-547-35	Sequence 35, Appl
5	130.4	14.0	2095	US-09-930-444-208	Sequence 208, App
6	130.4	14.0	2095	US-09-989-730-208	Sequence 208, App
7	130.4	14.0	2095	US-09-930-444-208	Sequence 208, App
8	130.4	14.0	2095	US-09-930-444-208	Sequence 208, App
9	130.4	14.0	2095	US-09-931-687-208	Sequence 208, App
10	130.4	14.0	2095	US-09-989-734-208	Sequence 208, App
11	130.4	14.0	2095	US-09-977-653-208	Sequence 208, App
12	130.4	14.0	2095	US-10-176-758-161	Sequence 161, App
13	130.4	14.0	2095	US-10-063-616-35	Sequence 35, Appl
14	130.4	14.0	2095	US-10-176-758-161	Sequence 161, App
15	130.4	14.0	2095	US-10-063-616-35	Sequence 35, Appl
16	130.4	14.0	2095	US-10-176-758-161	Sequence 161, App
17	130.4	14.0	2095	US-10-063-502-35	Sequence 35, Appl
18	130.4	14.0	2095	US-10-176-758-161	Sequence 161, App
19	130.4	14.0	2095	US-10-173-706-161	Sequence 161, App

ALIGNMENTS

RESULT 1
US-09-739-451-9
: Sequence 3, Application US/09719451
: Patent No. US2001002481A1
: APPLICANT: Eisner, Reinhard
: TITLE OF INVENTION: Dendritic and Brainiac-3
: FILE REFERENCE: P464
: PRIORITY DATE: 1998-03-12
: CURRENT FILING DATE: 2000-12-29
: PRIOR APPLICATION NUMBER: 09/213,364
: PRIORITY DATE: 1998-03-12
: PRIOR FILING DATE: 1998-03-12
: PRIOR APPLICATION NUMBER: 60/077,687
: PRIOR FILING DATE: 1998-03-12
: PRIOR APPLICATION NUMBER: 60/08,928
: PRIOR FILING DATE: 1998-11-17
: INVENTOR: Brainiac-3
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 9
: LENGTH: 1773
: ORGANISM: Homo sapiens

US-09-739-451-9
Query March 14.0% Score 130.4; DB 10; Length 1773;
Best Local Similarity 48.9%; Pred. No. 5; Ae-33;
Matches 387; Conservative 0; Mismatches 396; Indels 9; Gaps 1;
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RESULT 2

US 09-992-598-208
 Patent No. US2003016384A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi. J.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eskin, David L.
 APPLICANT: Fong, Sherman
 APPLICANT: Garber, Manispeiter
 APPLICANT: Gershtald, Mary E.
 APPLICANT: Godwin, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Kliner, Alvin L.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tamas, Daniel L.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Actins Encoding the Same
 FILE REFERENCE: P0730P1C20
 CURRENT APPLICATION NUMBER: US/09/992,598
 CURRENT FILING DATE: 2003-11-14
 PRIOR FILING DATE: 1998-06-16
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
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 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
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 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861

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 QY 882 ATACGCTGGCG 893
 Db 1274 CTTTGTGGCAG 1285
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 US-09-989-993A-208
 Sequence 208: Application US/09989293A
 GENERAL INFORMATION: 1644
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Desnoyers, Luc
 APPLICANT: Feron, Napoleon
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Geritsen, Mary E.
 APPLICANT: Goodman, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hargrave, David J.
 APPLICANT: Nisner, Mary A.
 APPLICANT: Pen, James
 APPLICANT: Paoni, Nicholas P.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tunes, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William J.
 APPLICANT: Zhang, Zhen
 TITLE OF INVENTION: Acids and Nucleoside and Nucleotide Polypeptides and Nucleoside
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P730P1066
 CURRENT APPLICATION NUMBER: US/09/989,293A
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-15
 PRIOR APPLICATION NUMBER: 60/052250
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065111
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-03-20
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 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908


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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P27301C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; PUBLICATION NO.: US2002019259A1
; CURRENT FILING DATE: 2002-05-02
; PRIORITY DATE: 2002-05-02
; SEQ ID NO 350: 170
; LENGTH: 2095
; TYPE: DNA
; ORIGIN: Homo Sapien
US-10-063-547-35

Query Match 14 94; Score 130.4; DS 9; Length: 2095;
Similarity 41.9%;
Matches 387; Conservative 0; Mismatches 356; Indels 9; Gaps 1;

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Oy 171 GCTTCCTCTCTCTGTGTGATCATCTGCGACACAGCTGCTGAGCTGTGCTATCC 210
Oy 544 TCTTCTGCTCTCTGTGATCATCTGCGACACAGCTGCTGAGCTGTGCTATCC 613
Oy 231 GCTTCCTCTCTGTGATCATCTGCGACACAGCTGCTGAGCTGTGCTATCC 290
Oy 614 GAGTACTCTGGGTGAAAATATCTGTGGGGATAGAGTCTTACATCTTTCTAT 673
Oy 291 TGCGACACACACAGCTGCGACGACACAGAGG-----TGCGACAGAGAGC 341
Oy 674 TAGCGACAGAGGCTGAAAGAGACAAATGTTGCGATGTCTTAGAGATGACACCC 733
Oy 342 AGCCACAGCGCGGATATCTGACAGAGATTTCTAGAGGCTATTAAGATCTGACCTG 401
Oy 734 TCTTATGTGTGACATATCCAGAGATTTTTTATGACATATATAAATCTGACCTGA 793
Oy 402 AGACATGATGGGTAGATGCTGCTCTTGTGCTCAGCGCGGCTGTGTGATGA 461
Oy 794 AACATCATATGCGATTCAGTGGGTAACTGATGATCTGATGATCTGATGATCTG 853
Oy 462 AACACAGCTCAGAGATTCATGATGATGATGATGATGATGATGATGATGATGAT 521
Oy 854 AGACACAGACTGATGTTTTTATCATATATATATGCGAATTAGAGAGTATCTTT 913
Oy 522 AACACACAGACTGATGTTTTTATCATATATATGCGAATTAGAGAGTATCTTT 581
Oy 914 ACACACTCAGAGATGTTTTTATCATATATATGCGAATTAGAGAGTATCTTT 973
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Oy 974 TTTACAAAACACACATATTTCTTACCGAGATGATCTTTTACAGTGTGCTCTCA 1033
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RESULT 5

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US-09-989,735-208
; PUBLICATION NO.: US2002019259A1
; GENERAL INFORMATION: US/09/989,735
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Fong, Sherman
; APPLICANT: Garber, Hanspeter
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Kijewski, Paul J.
; APPLICANT: Kijewski, Paul J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; PUBLICATION NO.: US2002019259A1
; CURRENT FILING DATE: 2002-05-02
; PRIORITY DATE: 2002-05-02
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-26
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/086706
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087755
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029

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Db 614 GAGTCTACTGGGCTGAAAAGAGTCTGGTGGGAGATGAGGTCTCTACNTTCTCTAT 733
 Qy 291 TGGGACACACCAAGCTGCTGACGGAAACAGAGG-----TGGACAGGAGACCC 341
 Db 674 TAGCGCAAGAGCGTAAGAGGAGCAAAAGTGTGGCAATGTGCTCTTAGAGATGAGACCC 733
 Qy 342 AGCAGACAGGGGAGGATATATGAGAGATATTCCTAGAGGCTATACATCTGACCTGA 401
 Db 734 TCTCTTATGCTGACATATCCGACAGATTTTATAGCAGATATATAAATCACTGACTGA 793
 Qy 402 AAAATATATAGGCGATAGAGAGAGGCTGCACTGTTTCTCTAGGGGGGCTTTGTGATGA 461
 Db 736 AAAATATATAGGCGATAGAGAGAGGCTGCACTGTTTCTCTAGGGGGGCTTTGTGATGA 461
 Qy 462 AAAAGAGCTGAGAGATGATATATATATGATGATATCTGCTGAGCTGCTGAGAGAA 521
 Db 854 AGAGACACACTGATGTTTTCATCATATAGCAATTTAGTAGAGTATCTTTTAACTGA 913
 Qy 522 ACAGAGACAGAGGTTTTCAGAGGTTATCCCTAAATTCAGATATCTGCTGAGAGAG 581
 Db 914 ACACATCAAGAGAGTTTTCAGAGGTTATCCCTAAATTCAGATATCTGCTGAGAGAG 581
 Qy 582 CATTGACAGATGCTGCTGATGATATTAATCTGATGATATGCTGGGAGTACAGAGATCT 641
 Db 974 TTTCAAAAACACCACTGATTTTACAGAGATATCTTACAGGTGCTCCCTCACTACT 1033
 Qy 642 GTGCGGACAGCTGAGCTGTTTCTGCGAGAGCGGAGATGAGCTGATATATGCTCCA 701
 Db 1034 CGAGTGGTGGTGTATATATGATGTCAGAGATTTGTCCCAAGATATCTGAATGATCG 1093
 Qy 702 AGAGGCTGCTGATATTAATCTGAGAGAGGATGTTGTGGGCTGCTGCTGAGAGAGCT 761
 Db 1094 GTGCACTGAAACCACTGATTTGAAGATGTTTATGCTGGGATCTGTTTGAATTTATTA 1153
 Qy 762 ACATGAGATGAGAGGATCTGATCCAGCCAGCTTTTTCAGGGGGTTAGCTGCT 821
 Db 1154 AAGTGAAGATCTATATTCAGAGAGCAAAATCTTTCTCTATATAGATCTCATTTGG 1213
 Qy 822 CGGATGCTCTTCAGAGAGATGCTGCTGCACTCATCAAGCTCGGACTGCTGGTG 881
 Db 1214 ATCTGCTCAACTGAGAGCTGTGATGTCAGCCATGCTTTTCTCAGAGGAGATCA 1273
 Qy 882 ACTATCTGGAGG 893
 Db 1274 CTTTITGGGNG 1285

1 APPLICANT: Williams, P. Mickey
 2 APPLICANT: Wood, William I.
 3 APPLICANT: Zhang, Zemin
 4 TITLE OF INVENTION: Selected and Transmembrane Polypeptides and Nucleic
 5 FILE REFERENCE: P270P1C19
 6 CURRENT APPLICATION NUMBER: US/09/990,444
 7 PRIOR APPLICATION NUMBER: 60/043787
 8 PRIOR FILING DATE: 1997-06-16
 9 PRIOR APPLICATION NUMBER: 60/062250
 10 PRIOR FILING DATE: 1997-11-12
 11 PRIOR APPLICATION NUMBER: 60/065186
 12 PRIOR FILING DATE: 1997-11-12
 13 PRIOR APPLICATION NUMBER: 60/065311
 14 PRIOR FILING DATE: 1997-11-24
 15 PRIOR APPLICATION NUMBER: 60/066770
 16 PRIOR FILING DATE: 1997-11-24
 17 PRIOR APPLICATION NUMBER: 60/075945
 18 PRIOR FILING DATE: 1998-03-20
 19 PRIOR APPLICATION NUMBER: 60/083322
 20 PRIOR FILING DATE: 1998-03-20
 21 PRIOR APPLICATION NUMBER: 60/084600
 22 PRIOR FILING DATE: 1998-05-07
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 64 PRIOR FILING DATE: 1998-06-10
 65 PRIOR APPLICATION NUMBER: 60/088824
 66 PRIOR FILING DATE: 1998-06-10
 67 PRIOR APPLICATION NUMBER: 60/088826

RESULT 6

US-09-990-444-208
 1 Publication No. US2002019300A1

2 GENERAL INFORMATION:

3 APPLICANT: Aikenzi, Avi J.

4 APPLICANT: Desnoyers, Luc

5 APPLICANT: Botstein, David

6 APPLICANT: Pilon, Benoit

7 APPLICANT: Fong, Sherman

8 APPLICANT: Gerber, Hanspeter

9 APPLICANT: Goddard, Audrey E.

10 APPLICANT: Godowski, Paul J.

11 APPLICANT: Grimaldi, J. Christopher

12 APPLICANT: Kijewski, J.

13 APPLICANT: Napier, Mary A.

14 APPLICANT: Pan, James

15 APPLICANT: Roy, Margaret Ann

16 APPLICANT: Stewart, Timothy A.

17 APPLICANT: Tunes, Daniel

18 APPLICANT: Wacholder, Colin K.

Db 1034 GCAGTGGGTGGTATATATATGTCGAGAGTTGGTCCAGAGATCTGAAGTATGCG 1093
 QY 1070 AGAGCTGCTACATCAATTCAGAGAGAGTGTGTGGGTCTGCTCCAGAGCGTGA 761
 Db 1094 GTCAGTCAACCAACCTCAAGTTCAGAGAGAGTGTATGTGGGATCTGTTGATTA 1153
 QY 762 ACATGAGATGAGAGAGCTCCATCCGACCGACCTTTTTCAGAGGCGCTAGAGCTCT 821
 Db 1154 AAGTGAACATCATATTCAGAGAGAGCAATATTTCTGTCATATAGATCAATCTGG 1213
 QY 822 CGTATGCTGCTTGAGAGAGATGCGCTGCGCATCTATCAAGCTCGAGACTCTGTG 881
 Db 1213 ATGCTGTCACATGAGAGAGTGTATGTCAGGCGATGGTCTTCTCCAGAGAGATCA 1273
 QY 882 ACTACTGCGAGCG 893
 Db 1274 CTATTTCGACGG 1285

RESULT 7

US-09-989-730-208

Sequence 208, Application US/09898730

Accession Number: US02019767A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Berman, David J.

APPLICANT: Desrochers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Harlow, E. W.

APPLICANT: Napier, Mary J.

APPLICANT: Pat, James

APPLICANT: Pooni, Nicholas F.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

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APPLICANT: Zhang, Zemin

APPLICANT: Zhang, Zemin

PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
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 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089603
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089601

1 APPLICANT: Eaton, Dan L.
 2 APPLICANT: Ferrara, Napoleone
 3 APPLICANT: Fong, Sherman
 4 APPLICANT: Gertzel, Mary E.
 5 APPLICANT: Goddard, Audrey
 6 APPLICANT: Godowski, Paul J.
 7 APPLICANT: Gurney, Austin L.
 8 APPLICANT: Kijavini, Ivar J.
 9 APPLICANT: Kuznetsov, Mary A.
 10 APPLICANT: Paoletti, Nicholas F.
 11 APPLICANT: Roy, Margaret Ann
 12 APPLICANT: Sauer, Timothy A.
 13 APPLICANT: Tamas, Daniel
 14 APPLICANT: Watanabe, Colin K.
 15 APPLICANT: Williams, P. Mickey
 16 APPLICANT: Zhang, Xian M.
 17 APPLICANT: Zhang, Xian M.
 18
 19 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 20 ACIDS Encoding the Same
 21 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 22 ACIDS Encoding the Same
 23 CURRENT APPLICATION NUMBER: US/09/930.436
 24
 25 PRIOR FILING DATE: 2001-11-14
 26 PRIOR APPLICATION NUMBER: 60/049787
 27 PRIOR FILING DATE: 1997-10-17
 28 PRIOR APPLICATION NUMBER: 60/062250
 29 PRIOR FILING DATE: 1997-11-13
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 35 PRIOR FILING DATE: 1998-02-25
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 99 PRIOR FILING DATE: 1998-06-05
 100 PRIOR APPLICATION NUMBER: 60/088202

[illegible][illegible]

GenCore version 5.1.4_p5.4278
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ON nucleic - nucleic search, using sw model

Run on: April 11, 2003, 14:22:18 ; Search time 1528.4 seconds
(without alignments)
15994,713 Million cell updates/sec

Title: US-09-914-152-2_COPY_492_1331

Perfect score: 840

Sequence: 1 tttcaasacagctctgtt.....gggaagatgcgcgcgc 840

Scoring table: INEXTRV.WUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1455102678 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

GenBank:

1: gb-hg.*

2: gb-hg.*

3: gb-hg.*

4: gb-hg.*

5: gb-hg.*

6: gb-hg.*

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8: gb-hg.*

9: gb-hg.*

10: gb-hg.*

11: gb-hg.*

12: gb-hg.*

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15: gb-hg.*

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22: gb-hg.*

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29: gb-hg.*

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39: gb-hg.*

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41: gb-hg.*

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	2	840	100.0	2762	9	AB020137	Homo sapi
2	3	840	100.0	2775	6	E38419	Homo sapi
3	4	840	100.0	10562	6	E38420	Novel poly
4	5	840	100.0	10562	6	E38420	Novel poly
5	6	840	100.0	140000	9	AB031980	Homo sapi
6	7	835.8	99.5	913	9	NSA6078	Homo sapi
7	8	835.8	99.5	913	9	NSA6078	Homo sapi
8	9	809.8	96.3	1376	9	AB041416	Homo sapi
9	10	789.2	94.0	1565	9	AB041413	Homo sapi
10	11	785.6	93.5	1566	9	AB041414	Homo sapi
11	12	763.6	93.0	1360	9	AB041412	Homo sapi
12	13	763.6	93.0	1360	9	AB041412	Homo sapi
13	14	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
14	15	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
15	16	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
16	17	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
17	18	420.8	38.2	17866	2	AC120346	Mus muscu
18	19	420.8	38.2	17866	2	AC120346	Mus muscu
19	20	420.8	38.2	17866	2	AC120346	Mus muscu
20	21	420.8	38.2	17866	2	AC120346	Mus muscu
21	22	420.8	38.2	17866	2	AC120346	Mus muscu
22	23	420.8	38.2	17866	2	AC120346	Mus muscu
23	24	420.8	38.2	17866	2	AC120346	Mus muscu
24	25	420.8	38.2	17866	2	AC120346	Mus muscu
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42	43	420.8	38.2	17866	2	AC120346	Mus muscu
43	44	420.8	38.2	17866	2	AC120346	Mus muscu
44	45	420.8	38.2	17866	2	AC120346	Mus muscu
45	46	420.8	38.2	17866	2	AC120346	Mus muscu

ALIGNMENTS

Result	No.	Score	Match	Length	DB	ID	Description
1	2	840	100.0	2762	9	AB020137	Homo sapi
2	3	840	100.0	2775	6	E38419	Homo sapi
3	4	840	100.0	10562	6	E38420	Novel poly
4	5	840	100.0	10562	6	E38420	Novel poly
5	6	840	100.0	140000	9	AB031980	Homo sapi
6	7	835.8	99.5	913	9	NSA6078	Homo sapi
7	8	835.8	99.5	913	9	NSA6078	Homo sapi
8	9	809.8	96.3	1376	9	AB041416	Homo sapi
9	10	789.2	94.0	1565	9	AB041413	Homo sapi
10	11	785.6	93.5	1566	9	AB041414	Homo sapi
11	12	763.6	93.0	1360	9	AB041412	Homo sapi
12	13	763.6	93.0	1360	9	AB041412	Homo sapi
13	14	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
14	15	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
15	16	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
16	17	502.2	59.8	927	10	AF254738	AB041412 Gorilla 9
17	18	420.8	38.2	17866	2	AC120346	Mus muscu
18	19	420.8	38.2	17866	2	AC120346	Mus muscu
19	20	420.8	38.2	17866	2	AC120346	Mus muscu
20	21	420.8	38.2	17866	2	AC120346	Mus muscu
21	22	420.8	38.2	17866	2	AC120346	Mus muscu
22	23	420.8	38.2	17866	2	AC120346	Mus muscu
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Pred. No. is the number of results predicted by chance to have a

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Search completed: April 11, 2003, 20:24:54
Job time : 1966.4 secs

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 DB 311 AGGACACAGGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370
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 DB 371 AAGACACAGGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
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 QY 731 GGTATGGTCTCTGAGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 790
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 DB 1274 CTTTGTGGAGAG 1285

RESULT 9

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Db 826 GCGGNGGNGGNGGNTAGTGNATGWSNNGNGGNGKNGTNGGNGNGNYTNCAGGCHATATG 885
QY 610 AAGAGGCTCCATACATTAACTGGAAGAGCGTGTGTGGGGCTGCTGCTCGAAGGCTG 669
Db 886 GAGCAGCGCAGATYNTYNSNATGAGTGNATYTTGTAGGATGCTGTTNGGNGNTN 945
QY 670 AACATCAG 577
Db 946 GGNVTMS 953

Search completed: April 11, 2003, 20:07:43
Job time : 159.586 secs

[illegible]


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(destroyed). Site:2: NotI; RNA source male hippocampus.
Library is oligo-dT primed and directionally
cloned. Insert size range 0.4-1.0 kb. Average
insert size 1.4 kb. Insert size range 0.9-1.4 kb. Library is
normalized and enriched for full-length clones and was
sequenced on a 0.1% Gruber (Invitrogen). Research Genetics
t38klnv code 012.
BASE COUNT      364 a 239 c 238 g      319 t      1 others
ORIGIN
      13.0% Score 109.4; db 13; Length 1101;
      Best Local Similarity 51.4%; Pred. No. 4.5e-20;
      Matches 285; Conservative 0; Mismatches 261; Indels 9; Gaps 1;
QY  20 TTTCAGACAGACGGGACTCTTANGTCCAGATACAGACTGCGACGAGACCTC 79
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QY  222 TTTCAGACAGACCTTTCACCTTCACACTTGGAGGACATCAACTGCTCTCATCAATC 281
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QY  80 CTCTCTGCTGCTGCTGACCTCATCCGACACACAGTTGCTGAGCGCATGGCCATCC 139
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QY  282 CATTTCTGCTGCTATCTGGTGAAGTCCGACCCCTTCAGATGTGAAGCGACGCGGCTTA 341
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QY  140 GCGACAGCTGGGGGAAGAGAGATGTTGAGCGAAGAGGCTGACAGACATCTTCTCTCC 199
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QY  342 GAGTTACTTGGGCTGAAAAAAGTCTTGGTGGGATATGAGGCTCTTACATTTTTCTTAT 401
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QY  200 TGGGGACACACAGCTGCGAGGGAACGAGAGG-----TGGACAGAGAGGCC 250
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QY  402 TGGCCCMAGAGGCTGAAAAGAGAGCAAAATGTGGCTTGTCTTAGAGATGAACCC 461
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QY  251 AGCAGACGGGCGCATATCCAGAGGATTCCTAGAGGCTCTATTACATCTGACCTGA 310
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QY  462 TCTTTATGTGACATATTCGACACAGATTTTATAGACACATATATATCCTGACTTGA 521
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QY  311 AGACATGATGGCATAGATGGGCTGCTGCTTGTCTCAGCGGGGCTTGTGATGA 370
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QY  522 CACCATATATGGCATACAGTGGGTAACTGTTTGGCCCATGCGCATGACTGATGA 581
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QY  371 AAACAGCTACGACATGTTATCAATGTTGACTATCTGACTGACTGCTCTGTGAGAAA 430
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QY  582 AGACACACATGATTTTCTCATCACTACCTGCGCATTTAGTGAATATCTTTAAACCTAA 641
DB  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  431 ACAGACACAGGTTTTTCACTGGCTTTGAACTCAATGAGTTCCCATCAGCGAGC 490
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QY  642 ACACCTCAGAGAGTTTTTCAGAGGTTATCCCTTAATGTATATATATCTCATAGAGT 701
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QY  491 CATTCAGCAAGTGTGTGAGTAAATCGATATCGTGGGACGAGTACCACTATCT 550
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QY  702 TTTCACAAAACCCCAATTTCTTACCMGAGTATCCTTCAGGGGCTTCCTCATACT 761
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QY  551 GTCCTCGGACCGGCT 565
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QY  762 CGACGGGTAGGGCT 776
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Search completed: April 11, 2003, 22:37:31
 Job time : 942.165 secs

TELEPHONE: (703)836-5300
TELEFAX: (703)683-4109
INSTRUMENT: ABI PRISM 577
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
TOPLOGY: linear
IMMEDIATE SOURCE: GenBank
CLONE: pTZ19-Fla
US-09-459-133-14

Best Local Similarity 4.5% Score 41.4; DB 1; Length 7218;
Matches 36; Conservative 18; Mismatches 178; Indels 0; Gaps 0;

Qy 44 TTATGCTCCAGATACAGATGATGAGCAGACATCTCTCTGCTGCTGCTGATCT 103
Db 1516 TTAGCTTTCTTAAAGAGGCTATGAGCATCTGTAATTAATCTATCTTAAAGAGTGA 1457
Qy 104 CATCCCAACAAATGCTGAGCGCATGCGCAGATGCGAGGAGGAGGAGGA 163
Db 1456 AAGATGAAAGATTTGTAACRHRHRHRHRHRHRHRHRHRHRHRHRHRHR 1397
Qy 164 TGTGTAAGAGACAGCTGAGACATCTCTCTGCTGCGACACAGCAGCAGCG 223
Db 1396 HR 1337
Qy 224 AAGCAAGAGGTGACAGCAGAGCAGCAGCAGCGGACATATCCAGAGATTC 289
Db 1398 AHR 1277
Qy 284 TAGACGTCTATTACATCTGACCTGAGCAGCATGCGCATGATGCTGCTGCT 343
Db 1276 HR 1217
Qy 344 TTCTGCTCAGCGCGCTGTTGATGAAGACAGCTGACATGCTCATATGCT 403
Db 1275 PRHR 1157
Qy 404 ATTCGATGACTGCTCTGAGAAAGACAGCAGCAGCAGCAGCAGCAGCAGC 444
Db 1156 PRHR 1116

Best Local Similarity 4.5% Score 37.4; DB 4; Length 6503;
Matches 77; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 61 GACTCGACGACACATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 4197 GCGCCGACGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4138
Qy 121 GCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 4131 ACTGCTTTGMAAATCTGACCCGACGATGCGGACGATGATGAGGAGCAGCAG 4078
Qy 181 CTGACGACATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
Db 4077 ATGACGACATGCTTCCCATGCGG 4055
RESULT 10
US-09-007-005-17
Sequence 17 Application US/0907005B
Patent No. 6255158
GENERAL INFORMATION:
APPLICANT: Spontak, Jack W.
INVENTOR: Spontak, Richard W.
APPLICANT: Liu, Rina
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
CURRENT APPLICATION NUMBER: US/09/007-005B

Best Local Similarity 46.5% Pred. No. 0.0096;
Matches 142; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
Qy 79 CTTCT 138
Db 524 CTTCT 583
Qy 139 CGCAGCAGCTGGGAGGAGGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 198
Db 584 AGGAGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 411
Qy 399 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 258
Db 644 CTAGG---AAGGGGGGGCTGACTTAGATGATCTAGATGATGAGGAGGAT 700
Qy 255 GGGAGCATATCCCAAGAGATTTCTGATAGCTGCTATTAATCTGACCTGAGAC 318
Db 701 GGTACTGATCTTGGGACTTCTGATGATGCTTCTCTTAAAGGAGCATCAN 760
Qy 319 ATGGGATAGATAGGCTGATCTTTGCTCTGAGGCGGCTTGTGATGAA 371
Db 761 CTCTCTGACTGCTGAGCAGCAGCTGCGGATCTTAATTTTCTCTCTCT 813

RESULT 9
US-09-404-650-12/C
Sequence 12, Application US/0940450
Patent No. 6309558
GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
INVENTOR: Dietrich, Paul S.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: K0043B-AB2 Sequence Listing
FILE REFERENCE: K0043B-AB2 Sequence Listing
CURRENT APPLICATION NUMBER: US/09/404-650
CURRENT FILING DATE: 1999-09-23
INSTRUMENT: ABI PRISM 577
SEQUENCE: Patent Ver. 2.0
SEQ ID NO 12
LENGTH: 6503
ORGANISM: Rattus sp.
US-09-404-650-12

Best Local Similarity 53.8% Pred. No. 0.18;
Matches 77; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 61 GACTCGACGACACATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 4197 GCGCCGACGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4138
Qy 121 GCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 4131 ACTGCTTTGMAAATCTGACCCGACGATGCGGACGATGATGAGGAGCAGCAG 4078
Qy 181 CTGACGACATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
Db 4077 ATGACGACATGCTTCCCATGCGG 4055
RESULT 10
US-09-007-005-17
Sequence 17 Application US/0907005B
Patent No. 6255158
GENERAL INFORMATION:
APPLICANT: Spontak, Jack W.
INVENTOR: Spontak, Richard W.
APPLICANT: Liu, Rina
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
CURRENT APPLICATION NUMBER: US/09/007-005B

RESULT 11
 US-09-044-796-17
 Application US/09244796
 Patent No. 6281144
 1 GENERAL INFORMATION:
 2 APPLICANT: Scottak, Richard W.
 3 APPLICANT: Liu, Rhee
 4 APPLICANT: Liu, Rhee
 5 TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 6 TITLE OF INVENTION: FUSIONS
 7 CURRENT APPLICATION NUMBER: US/09/244,796
 8 CURRENT FILING DATE: 1999-02-05
 9 EARLIER APPLICATION NUMBER: 60/035,963
 10 EARLIER FILING DATE: 1997-08-23
 11 EARLIER APPLICATION NUMBER: 60/064,493
 12 EARLIER FILING DATE: 1997-11-06
 13 EARLIER APPLICATION NUMBER: 09/007,005
 14 EARLIER FILING DATE: 1998-01-14
 15 NUMBER OF SEQ ID NOS: 33
 16 SOFTWARE: FastSD for Windows Version 4.0
 17 SEQUENCE LENGTH: 269
 18 TYPE: RNA
 19 ORGANISM: Artificial Sequence
 20 OTHER INFORMATION: Translation template
 21 FEATURE:
 22 NAME/KEY: misc_feature

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 Db 1214 ATGCTGTCGCACTCAAGCTGATTCGACCCGCTTGGCTTTCTTCGAGAGATCA 1273
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 Db 1274 CTTTTCGACG 1285
 RESUB: 3
 US-09-989-293A-208
 : Sequence 208. Application US/0989293A
 : Patent No. US20020171641
 : APPLICANT: Ashkenazi, Avi J.
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Rotstein, David
 : APPLICANT: Etkin, Dan L.
 : APPLICANT: Ferrare, Napoleone
 : APPLICANT: Fogel, Sherman
 : APPLICANT: Gerzhen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Hochstadt, Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Kijavits, Ivar J.
 : APPLICANT: Kijavits, Alexander A.
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Scharf, Anthony A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Watanabe, Colin K.
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Zhang, Zemin
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 : FILE REFERENCE: US0989293A encoding the Same
 : CURRENT APPLICATION NUMBER: US/09/989,293A
 : CURRENT FILING DATE: 2001-11-20
 : PRIOR FILING DATE: 1997-06-10/049787
 : PRIOR APPLICATION NUMBER: 60/062250
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/065186
 : PRIOR FILING DATE: 1997-11-12/065186
 : PRIOR APPLICATION NUMBER: 60/065311
 : PRIOR FILING DATE: 1997-11-13
 : PRIOR APPLICATION NUMBER: 60/066770
 : PRIOR FILING DATE: 1997-11-13
 : PRIOR APPLICATION NUMBER: 60/075945
 : PRIOR FILING DATE: 1998-02-25
 : PRIOR APPLICATION NUMBER: 60/078910
 : PRIOR FILING DATE: 1998-03-20
 : PRIOR APPLICATION NUMBER: 60/083322
 : PRIOR FILING DATE: 1998-04-28
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 : PRIOR FILING DATE: 1998-05-07
 : PRIOR APPLICATION NUMBER: 60/087106
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 : PRIOR FILING DATE: 1998-06-02
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 : PRIOR FILING DATE: 1998-06-10
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 : PRIOR FILING DATE: 1998-06-10
 : PRIOR APPLICATION NUMBER: 60/088858
 : PRIOR FILING DATE: 1998-06-11
 : PRIOR APPLICATION NUMBER: 60/088861
 : PRIOR FILING DATE: 1998-06-11
 : PRIOR APPLICATION NUMBER: 60/088876
 : PRIOR FILING DATE: 1998-06-12
 : PRIOR APPLICATION NUMBER: 60/089105
 : PRIOR FILING DATE: 1998-06-12
 : PRIOR APPLICATION NUMBER: 60/089440
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 : PRIOR APPLICATION NUMBER: 60/089598
 : PRIOR FILING DATE: 1998-06-17
 : PRIOR APPLICATION NUMBER: 60/089599
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 : PRIOR APPLICATION NUMBER: 60/089600
 : PRIOR FILING DATE: 1998-06-17
 : PRIOR APPLICATION NUMBER: 60/089653
 : PRIOR FILING DATE: 1998-06-18
 : PRIOR APPLICATION NUMBER: 60/089901
 : PRIOR FILING DATE: 1998-06-18
 : PRIOR APPLICATION NUMBER: 60/089907
 : PRIOR FILING DATE: 1998-06-18
 : PRIOR APPLICATION NUMBER: 60/089908
 : PRIOR FILING DATE: 1998-06-18

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2	PRIOR FILING DATE: 1998-06-04	2	PRIOR APPLICATION NUMBER: 60/088030	2	Matches: 387; Mismatches: 31; Caps: 1;
3	PRIOR FILING DATE: 1998-06-04	3	PRIOR APPLICATION NUMBER: 60/080355	3	20 TTTTACAGACAGCGAGTCTTGGCTTCCGATAGACATGAGCGACGACCTC 79
4	PRIOR FILING DATE: 1998-06-04	4	PRIOR APPLICATION NUMBER: 60/088033	4	Db 494 TTTTACAGACAGCTTTGCTTACGACTTCCGATAGACATGAGCGACGACCTC 553
5	PRIOR FILING DATE: 1998-06-04	5	PRIOR APPLICATION NUMBER: 60/083326	5	Qy 80 CTTCTCTCTCTGCTGGTGGATCTATCTCCACACAGAGTGGCTGAGCGACATGCGATCC 139
6	PRIOR FILING DATE: 1998-06-04	6	PRIOR APPLICATION NUMBER: 60/088167	6	Db 554 CATTCTCTGCTGATCTGGTGGATCTATCTCCACCTTCTGATGGAGGACGAGCGACGATTA 613
7	PRIOR FILING DATE: 1998-06-04	7	PRIOR APPLICATION NUMBER: 60/088202	7	Qy 140 GCGAGAGCTGGGGGAAGAGAGGATGGTGAAGGGAGGAGGATCTTCTCTCTCTCTCTCTC 359
8	PRIOR FILING DATE: 1998-06-05	8	PRIOR APPLICATION NUMBER: 60/088212		
9	PRIOR FILING DATE: 1998-06-05	9	PRIOR APPLICATION NUMBER: 60/088217		
10	PRIOR FILING DATE: 1998-06-05	10	PRIOR APPLICATION NUMBER: 60/088255		
11	PRIOR FILING DATE: 1998-06-05	11	PRIOR APPLICATION NUMBER: 60/088734		
12	PRIOR FILING DATE: 1998-06-10	12	PRIOR APPLICATION NUMBER: 60/088738		
13	PRIOR FILING DATE: 1998-06-10	13	PRIOR APPLICATION NUMBER: 60/088742		
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17	PRIOR FILING DATE: 1998-06-10	17	PRIOR APPLICATION NUMBER: 60/088858		
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19	PRIOR FILING DATE: 1998-06-11	19	PRIOR APPLICATION NUMBER: 60/088876		
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21	PRIOR FILING DATE: 1998-06-12	21	PRIOR APPLICATION NUMBER: 60/089440		
22	PRIOR FILING DATE: 1998-06-16	22	PRIOR APPLICATION NUMBER: 60/089512		
23	PRIOR FILING DATE: 1998-06-16	23	PRIOR APPLICATION NUMBER: 60/089514		
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25	PRIOR FILING DATE: 1998-06-17	25	PRIOR APPLICATION NUMBER: 60/089538		
26	PRIOR FILING DATE: 1998-06-17	26	PRIOR APPLICATION NUMBER: 60/089538		
27	PRIOR FILING DATE: 1998-06-17	27	PRIOR APPLICATION NUMBER: 60/089599		
28	PRIOR FILING DATE: 1998-06-17	28	PRIOR APPLICATION NUMBER: 60/089600		
29	PRIOR FILING DATE: 1998-06-17	29	PRIOR APPLICATION NUMBER: 60/089653		
30	PRIOR FILING DATE: 1998-06-18	30	PRIOR APPLICATION NUMBER: 60/089901		
31	PRIOR FILING DATE: 1998-06-18	31	PRIOR APPLICATION NUMBER: 60/089907		
32	PRIOR FILING DATE: 1998-06-18	32	PRIOR APPLICATION NUMBER: 60/089907		
33	PRIOR FILING DATE: 1998-06-18	33	PRIOR APPLICATION NUMBER: 60/089908		
34	PRIOR FILING DATE: 1998-06-18	34	PRIOR APPLICATION NUMBER: 60/089947		
35	PRIOR FILING DATE: 1998-06-19	35	PRIOR APPLICATION NUMBER: 60/089948		
36	PRIOR FILING DATE: 1998-06-19	36	PRIOR APPLICATION NUMBER: 60/089952		
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38	PRIOR FILING DATE: 1998-06-22	38	PRIOR APPLICATION NUMBER: 60/090252		
39	PRIOR FILING DATE: 1998-06-22	39	PRIOR APPLICATION NUMBER: 60/090254		

Db 1034 GAGATGGGTGGGTATATATATATCCAGAGATTTGGCCAGGAGTATCAATGATGAG 1093
 Qy 1091 AGAGGCTCCCATATCAATAGCTGGAGAGCTGTTGTGGGGCTCTCCCTCGAAGAGCTGA 670
 Db 1094 GTCAGCTAAAGACCCACAGCTTTCAGAGAGCTGTTGGAGAGCTGTTGAAATATATTA 1153
 Qy 671 ACATACAGATCCAGAGAGCTCCAGCCAGCACTTTTTCAGAGGGGCTTACGCTTCT 730
 Db 1154 AAGTGAAGATCATATCCAGAGAGACAGATCTTTCTTTCTTATGATAGCATATGG 1213
 Qy 731 CATTGAGCTCTTCAGAGAGATGGGCTGCACTTCAATCAAGCTCGCACTTCTGG 750
 Db 1213 AGTTCGCTGCTGCTGAGAGCTGATGTCAGAGCCAGGCTTTCTTCAGAGAGATCATCA 1273
 Qy 791 ACTACTGCGAGG 802
 Db 1274 CTTTTCGAGG 1285

RESUME 7

US-09-986-730-208

Sequence 208, Application US/0989730

Publication No. US2002019757A1

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Boischard, David

APPLICANT: Batson, Dan L.

APPLICANT: Ferreira, Napoléone

APPLICANT: Fong, Sharmaine

APPLICANT: Gerriksen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gorman, David

APPLICANT: Grunwald, Techristopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavitt, Ivay J.

APPLICANT: Kohn, Gary A.

APPLICANT: Pen, James

APPLICANT: Pen, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Schmitt, Kimberly A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730105

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 1997-06-11

PRIOR FILING DATE: 1997-06-11

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 7 PRIOR FILING DATE: 1998-06-17
 7 PRIOR APPLICATION NUMBER: 60/089653
 7 PRIOR FILING DATE: 1998-06-17
 7 PRIOR APPLICATION NUMBER: 60/089801

APPLICANT: Baton, Dan L.
 APPLICANT: Petrakia Napoléone
 APPLICANT: Bong, Sherman
 APPLICANT: Gagliardi, Joseph E.
 APPLICANT: Gerritsen, Nancy E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Goodwin, Jr., Paul
 APPLICANT: Goode, J. Christopher
 APPLICANT: Gurley, Austin L.
 APPLICANT: Hájvín, Ivar J.
 APPLICANT: Harlowe, John C.
 APPLICANT: Harper, Mary A.
 APPLICANT: Heisterkamp, Anthony A.
 APPLICANT: Hunn, Daniel
 APPLICANT: Kawanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Lammi, William M.
 APPLICANT: Zhang, Zhenlin

TITLE OF INVENTOR: Secreted and Transmembrane Polypeptides and Nucleic Acids
 FILING DATE: 07-19-2006; ENDING THE SAME
 CURRENT APPLICATION NUMBER: US/09/890,436
 PRIOR APPLICATION NUMBER: 60/049787
 CURRENT FILING DATE: 2001-11-14
 PRIOR FILING DATE: 1997-10-11
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 PRIOR APPLICATION NUMBER: 60/042250
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 PRIOR APPLICATION NUMBER: 60/088202
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[illegible]

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 4 PRIOR APPLICATION NUMBER: 60/088824
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 17 PRIOR FILING DATE: 1998-06-16
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 28 PRIOR APPLICATION NUMBER: 60/089801
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 36 PRIOR APPLICATION NUMBER: 60/089948
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 46 PRIOR APPLICATION NUMBER: 60/090355
 47 PRIOR FILING DATE: 1998-06-23
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 51 PRIOR FILING DATE: 1998-06-24
 52 PRIOR APPLICATION NUMBER: 60/090435
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 54 PRIOR APPLICATION NUMBER: 60/090445
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 56 PRIOR APPLICATION NUMBER: 60/090472
 57 PRIOR FILING DATE: 1998-06-24
 58 PRIOR APPLICATION NUMBER: 60/090535
 59 PRIOR FILING DATE: 1998-06-24
 60 PRIOR APPLICATION NUMBER: 60/090542
 61 PRIOR FILING DATE: 1998-06-24

Query Match: 15 5%; Score 130.4; DB 9; Length 2095.
 Percentages: Similarity 48.9%; Offset No. 28-33; Mismatches 387; Conservative 9; Gaps 1;
 Matched 387; Mismatched 396; Indels 9; Gaps 1;

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 DB 494 TTTCAGAGAGACTTCCTTAAGCTCCAGATACAGACTCCAGAGAGACTC 553
 QY 80 CTTCT 139
 DB 554 CATTCT 613
 QY 140 CCGACACTCGGAG 199
 DB 614 GAGTTCT 673
 QY 200 TGGGACACAG 750
 DB 674 TAGCCAG 733
 QY 251 AGGACAG 310
 DB 734 TCTTTATCT 793
 QY 311 AGACATATCGGAG 453
 DB 793 AGACATATCGGAG 793
 QY 371 AGACATATCGGAG 430
 DB 854 AGACATATCGGAG 913
 QY 431 AGACATATCGGAG 970
 DB 914 AGACATATCGGAG 973

Qy 491 CATTGACAGAGTGTTTCATGTAATCTGATATCTGGTGGACAGTACCGACAGTCT 550
 Db 974 TTATCAAAAACCAATATTTCTTACAGGATATCTCTTCAAGAGTCTCCCTCAACT 1033
 Qy 493 GCTGCGCCAGCCAGTGATGGTTTCTTGGAGAGTGGAGTGGATGATGATGTCCTCA 610
 Db 975 GCTGCGCCAGCCAGTGATGGTTTCTTGGAGAGTGGAGTGGATGATGATGTCCTCA 610
 Qy 1034 AGAGTGCTGCTGTTATATATCTCAAGATTTGGTGCAGAGTATCATGAATGATGG 1093
 Db 976 AGAGTGCTGCTGTTATATATCTCAAGATTTGGTGCAGAGTATCATGAATGATGG 1093
 Qy 611 AGAGTGCTGCTGTTATATATCTCAAGATTTGGTGCAGAGTATCATGAATGATGG 670
 Db 977 AGAGTGCTGCTGTTATATATCTCAAGATTTGGTGCAGAGTATCATGAATGATGG 670
 Qy 1094 GTCACTGATTAACCCATCATAGTTTATGTCAGATTTATGTCGAGGCTGTGTAATTAA 1153
 Db 978 ACATCAATATGAGAGTCTGATCCAGCCAGCTTTTTCGAGGCTGTGTAATTAA 1153
 Qy 671 ACATCAATATGAGAGTCTGATCCAGCCAGCTTTTTCGAGGCTGTGTAATTAA 1213
 Db 1154 ACATCAATATGAGAGTCTGATCCAGCCAGCTTTTTCGAGGCTGTGTAATTAA 1213
 Qy 731 CCGTGGGCTCTCAGGAGATGGTGGCTGCAGCTCATCAGCTGAGCTCTCTGG 790
 Db 979 CCGTGGGCTCTCAGGAGATGGTGGCTGCAGCTCATCAGCTGAGCTCTCTGG 790
 Qy 1214 ACTACTGTCAGAG 802
 Db 1274 CTTTTGGCAGG 1285

RESULT 12
 00:49:49:265-298
 00:49:49:265-298 Application US:09497653
 1 Publication No. US2003008297A1
 2 GENERAL INFORMATION:
 3 APPLICANT: Ashkenazi, Avi J.
 4 APPLICANT: Ashkenazi, P.
 5 APPLICANT: Botstein, David
 6 APPLICANT: Desnovers, Luc
 7 APPLICANT: Eaton, Dan I.
 8 APPLICANT: Fong, Sherman
 9 APPLICANT: Gerber, Hanspeter
 10 APPLICANT: Glickstein, Mary E.
 11 APPLICANT: Godowski, Paul J.
 12 APPLICANT: Grimaldi, J. Christopher
 13 APPLICANT: Klagsbrun, L.
 14 APPLICANT: Klagsbrun, M.
 15 APPLICANT: Napier, Mary A.
 16 APPLICANT: Pag, James
 17 APPLICANT: Pons, Nicholas P.
 18 APPLICANT: Pons, Michael Ann
 19 APPLICANT: Tumas, Daniel
 20 APPLICANT: Williams, Colin K.
 21 APPLICANT: Williams, P. Mickey
 22 APPLICANT: Wood, William I.
 23 APPLICANT: Zhang, Zemin
 24 TITLE OF INVENTION: Acids encoding the Same
 25 FILE REFERENCE: P2730P1C38
 26 CURRENT APPLICATION NUMBER: US/09/997,653
 27 PRIORITY DATE: 1997-06-16
 28 PRIORITY APPLICATION NUMBER: 60/049787
 29 PRIORITY FILING DATE: 1997-06-16
 30 PRIORITY APPLICATION NUMBER: 60/062250
 31 PRIORITY FILING DATE: 1997-11-12
 32 PRIORITY APPLICATION NUMBER: 60/065186
 33 PRIORITY FILING DATE: 1997-11-12
 34 PRIORITY APPLICATION NUMBER: 60/065311
 35 PRIORITY FILING DATE: 1997-11-24
 36 PRIORITY APPLICATION NUMBER: 60/075945
 37 PRIORITY FILING DATE: 1998-03-20
 38 PRIORITY APPLICATION NUMBER: 60/078910
 39 PRIORITY FILING DATE: 1998-03-20

1 PRIORITY APPLICATION NUMBER: 60/083322
 2 PRIORITY FILING DATE: 1998-04-28
 3 PRIORITY APPLICATION NUMBER: 60/084600
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 2 PRIOR APPLICATION NUMBER: 60/092182
 2 PRIOR FILING DATE: 1998-07-09

Query Match

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RESULT 13
US-10-174

Qy	671	ACATGAGATTGGAGAGCTTCACCTCCAGGCAACGCTTTTTCAGAGGGGCTTACGCTCTT	79	TTTACAGAGAGAGGAGGAGGAGCTCTTACGCTCCGACATAGACGACGAGGACACCTC	79	
Db	1154	AAGTGAATCATATTCGACAGAGAAATATCTTCTTCTATATAGATTCATTG	96	TTTACAGAGAGAGGAGGAGGAGCTCTTACGCTCCGACATAGACGACGAGGACACCTC	96	
Qy	731	CGATAGGCTCTTAGAGAGGATCGTGGCTCGACCTCATCAAGCTCGAGATCTCTTGG	79	CGTCTCTCTGCTCTGGTGGAGCTCTTCCACACAGTTGGCTGGAGGACGAGGACCTC	139	
Db	1214	AGTCTGTGAACCTGAGAGCTGATTCGACGACGCTCTTCCAGGAGATCATCA	127	CGTCTCTCTGCTCTGGTGGAGCTCTTCCACACAGTTGGCTGGAGGACGAGGACCTC	139	
Qy	791	ACTATGGCAGG 802		544	CGCAGATCGTGGGAGAGAGAGTGGTGAAGGACAGCTGAGACATCTTCCTCC	199
Db	1274	CTTTTTCGCGAG 1285		614	GATTTATTTGGGTGAAAAAGCTTGTGTGGGGAATNGAGTGTTCATCTTCTCAT	673
RESULT 14						
US-10-176-758-161						
: Sequence 161, Application US/10/176758						
: Publication No. US2003008355A1						
: APPLICANT: Baker, Kevin P.						
: APPLICANT: Chen, Jian						
: APPLICANT: Desnoyers, Luc						
: APPLICANT: Gadowski, Paul J.						
: APPLICANT: Gurney, Austin L.						
: APPLICANT: Pan, James						
: APPLICANT: Pardo, Gloria						
: APPLICANT: Natanabe, Colin K.						
: APPLICANT: Wood, William I.						
: APPLICANT: Zhang, James						
: TITLE OF INVENTION: ACIDS ENCODING THE SAME						
: FILE REFERENCE: P34301C104 US/10/176, 758						
: CURRENT FILING DATE: 2003-05-21						
: Prior Application Removed - See File Wrapper or Palm						
: NUMBER OF SEQ ID NOS: 612						
: SEQ ID NO: 161						
: LENGTH: 2095						
: TYPE: DNA						
: ORGANISM: Homo Sapien						
US-10-176-758-161						
Query Match 15.5%: Score 130.4; DB 9; Length 2095;						
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Matches 396: 0; Mismatches 396; Indels 9; Gaps						
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Db	614	GATTTATTTGGGTGAAAAAGCTTGTGTGGGGAATNGAGTGTTCATCTTCTCAT	673	GATTTATTTGGGTGAAAAAGCTTGTGTGGGGAATNGAGTGTTCATCTTCTCAT	673	
Qy	200	TGGGACAGAGGCTGTGAAGGAGAGAAATGTGGATATATAGACGACGACCTC	250	TGGGACAGAGGCTGTGAAGGAGAGAAATGTGGATATATAGACGACGACCTC	250	
Db	674	TAAAGCAGAGGCTGTGAAGGAGAGAAATGTGGATATATAGACGACGACCTC	733	TAAAGCAGAGGCTGTGAAGGAGAGAAATGTGGATATATAGACGACGACCTC	733	
Qy	251	AGGACAGAGGGGAGGATATTCACAGAGATTTCTTAGAGCTATTATCAATCTACCTCA	310	AGGACAGAGGGGAGGATATTCACAGAGATTTCTTAGAGCTATTATCAATCTACCTCA	310	
Db	734	TTCTTATATATATATCGACAGAGATTTTTTAGACAGATATATTAACCTGACCTCA	370	TTCTTATATATATATCGACAGAGATTTTTTAGACAGATATATTAACCTGACCTCA	370	
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Qy	371	AAAGAGATACAGATATGTCATATATATGACTATCTGACTGACGACGCTTTCGAGAA	430	AAAGAGATACAGATATGTCATATATATGACTATCTGACTGACGACGCTTTCGAGAA	430	

[illegible]

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Db 854 AGACAGACAGTATTTTCATCATCTGGCAATTTAGTGAATATCTTTTAACTTA 913
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Db 911 ACACATCAGAGAGATTTTTCATGAGTATCTCTGATATATATATCTATAGAGAT 973
Oy 494 CATTCAGAGAGTTTGTCTGAATCTGAATCTATGATCTGGGACAGCCACCATCT 550
Db 974 TTTACCAAAAACCATATCTTCTACAGAGATATCTCTCAAGGTGTCTCCCTACT 1033
Oy 551 GCTCGGACAGCGCTAGCTAGTGTCTTTCGAGAGCTGGAGCTAGCTGACATGTCTCA 1093
Db 1034 CGAGTGTGTGGTGTATATATGTCCTGACAGATTTGGTCCACAGATCTATGAATGAT 1093
Oy 611 AGAGCTCCCATCAATTAACCTGGAAGAGCTGTCTTGTGGGCTTCTGCTCGAAGAGCTGA 1153
Db 1094 GTCACTGAATTAACCATCAAGTTCGAGAGTGTATGTGGGAGTGTGTGAATTTATTA 1153
Oy 671 AONTGATAGTGAAGAGCTATCTCCACAGCGAGCTTTTTCAGAGGGGTTCACCTCT 730
Db 1154 AAGTGAACATCAATTCATCGAAGACAAATCTTCTCTCTATATGAATCATCTCTCT 1213
Oy 731 CGATAGCTGTCTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 790
Db 1214 ATGCTGTCACTAGAGAGCTGTCTTGTAGGCTGCTGCTGCTGCTGCTGCTGCT 1273
Oy 791 ACTATGCTGAG 802
Db 1274 CTTTGTGGAGG 1285

RESULT 15
US-10-063-616-35 Location US/10063616
Sequence 35 Applicant US/0001855A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Elivatroff, Ellen
APPLICANT: Elivatroff, E.
APPLICANT: Goldard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hatanaka, Colin K.
APPLICANT: Hatanaka, Colin K.
APPLICANT: Hatanaka, Colin K.
TITLE OF INVENTION: SECTORS INCLUDING THE SAME
FILE REFERENCE: P2320R1C1
CURRENT APPLICATION NUMBER: US/10/063-616
PUBLICATION DATE: 2002-05-03
PUBLICATION DATE REMOVAL: See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 35
INSTRUMENT: 495
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-616-35
Query Match 15.5%; Score 130.4; D8 9; Length 2095;
Best Local Similarity 48.9%; Pred. No. 28-33;
Matches 387; Conservative 0; Mismatches 396; Indels 9; gaps 1;
Oy 20 TTTACAGAGAGAGGAGCTTCTTAACTCCAGATCTGAGAGATCAATCACTGCTCATCAATAT 553
Db 494 TTTACAGAGAGAGCTTCTTAACTCCAGATCTGAGAGATCAATCACTGCTCATCAATAT 553
Oy 80 CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 139
Db 554 CATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
Oy 140 GCGAGAGCTGGGGGAAGAGAGATGTGGAGGGAACAGCTGAGAGATCTTCTCTCC 199
Db 614 GAGTACTGTGGGGTGAAMAAAAGTGTGGTGGGAGATAGAGTCTTCACTTCTTCTAT 673

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Oy 200 TGGGGACACAGCATGATGCTGAGCGAGAGCAAGAGG -----TGGACAGAGAGAGC 250
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Oy 251 AGCAGACAGGGAATATCTCAGAGAGGATTTCTAGAGAGTCTATTACATCTGCACCTGA 310
Db 734 TCTTTATGAGATATCTCCAGACATTTTATAGACACATATATTAACCTGCATCTGA 793
Oy 311 AGACATGATGGGATAGATATGGTCCATGCTTTTGTGCTCAGCGGGGCTTGTGATGA 370
Db 794 AAGCATATTGCAATCAAGTGGGTACTGAGTTTGGGCGCAATGCAAGTAGTAGTATGA 853
Oy 371 AAGCACTCAGACAGATTTTCAATCATATGTGATATCTGACTGAGCACTGCTCTGAAGAAA 430
Db 854 AGCAACACATGATATTTTCACTGCTCTTCACTGAGTCTGCTGCTTCTTAACTCTTA 913
Oy 431 ACAGACACAGGCTTTTTCATGCTCTTCACTGAGTCTCAATGAGTATGCTCATAGCAG 490
Db 914 CAATCAAGAGTGGTTTGTCAATCAATCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 973
Oy 491 GCTCGGACAGCGCTAGTGTCTTTCGAGAGCTGTCTTGTGGGCTGCTGCTGAGAGCTGA 550
Db 974 TTTACCAAAAACCATATCTTCTACAGAGATATCTCTCAAGGTGTCTCCCTACTCT 1033
Oy 551 GCTCGGACAGCGCTAGTGTCTTTCGAGAGCTGTCTTGTGGGCTGCTGCTGAGAGCTGA 610
Db 1034 GCAATGCTGTGGTGTATATATGCTCAGAGATTTGTCAGAGATCTATGATCATGAG 1093
Oy 611 AGAGCTCCCATCAATTAACCTGGAAGAGCTGTCTTGTGGGCTGCTGCTGAGAGAGCTGA 670
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Db 1154 AAGTGAATCTCAATTCAGAGAGACAAATCTTCTCTCTCTCTCTCTCTCTCTCTCT 1213
Oy 731 CGATAGCTGTCTGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 790
Db 1214 ATGCTGTCACTAGAGAGCTGTCTTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1273
Oy 791 ACTATGCTGAG 802
Db 1274 CTTTGTGGAGG 1285

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Job time : 05:14:36 secs

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[illegible]

[illegible]

[illegible]

Genetics, Laboratory of Evolutionary Genetics; Illi Yata, Mishima,
Shizuoka 411-8540, Japan (E-mail:nsaitougens@ng.ac.jp,
USL:tokyo@yayoi.lab.ng.ac.jp/silver/, Tel:81-559-81-6790,
Fax:81-559-81-6789)
Location/Qualifiers
1. 1570

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Query Match 11.6%; Score 321; DB 9; Length 1570;
Best Local Similarity 98.9%; Pred. No. 3,3e-176;
Matches 771; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

[illegible]

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912 AATGAGGAGTGTGGAGGAAGGACGTGAAGACATCTTCTCTGSGGACCCACG 971
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[illegible]

1091 GTCATCGCTTTTGCTCTGAGCGGTTTGATGAACAACAGATCAGACATGTTGATC 1150

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945	GCCTTCTCGAACTCAATGAGTGTTCACATCAGCAGCAGCATTCAGCAAGTGGTGTTCAGT	1004
1211	GCCTTCTCGAACTCAATGAGTGTTCACATCAGCAGCAGCATTCAGCAAGTGGTGTTCAGT	1270
1005	AAATCTGAAATATCGTGGGACAGTACCCACATCTCTCCGCGACCGCGCTACGCTGTT	1064

DB	1271	AAATCTGATATATCCGTGGGACAGTACCGCCGATCTCTCCGGCAGCCGCTACGTGTTT	1330
OY	1065	TCGCGCAGCGCGGAGTCACAGTGTACATATGTCCTCAGAGGCTCCCATACATTAACCTG	1124
DB	1331	TCGCGCAGCTGGCGAATCTAGGTGTATCATGTCTCTCCGAGAGCGCTCCCATACATTAACCTG	1390

OY 1125 GAAGACGTTTGTGGGCTCTGCCTCGAAAGCTGAACATCAGATTGGAGGAGCTCCAC 1184
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DB 1391 GAAGACGTTTGTGGGCTCTGCCTCGAAAGCTGAACATCAGATTGGAGGAGCTCCAC 1450

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DB		
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AB01414				
LOCUS				
DEFINITION				
pan troglodytes beta1,3-galT 5' gene for UDP-Gal:GlcNAc				
beta1,3-galactosyltransferase 5, partial cds.				

AB041414.1 GI:7591022
Pan troglodytes (isolate:chimp-202) DNA.
Pan troglodytes
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
1 (bases 1 to 1566)
[J. V. and Saitou, N.]

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE
Silver Project		Published Only in Database (2000)		
2 (bases 1 to 1566)				
Liu, Y. and Saitou, N.				
Direct Submission				

Genetics, Laboratory of Evolutionary Genomics, Ili Yeta, Mishima, Shizuoka 411-8540, Japan (E-mail: insaito@genomics.nig.ac.jp, URL: <http://sayer.lab.nig.ac.jp/~silver/>; Tel: 81-559-81-5790, Fax: 81-559-81-6789)

FEATURES Location/Qualifiers
1. 1586
source

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CDS
575..1566
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Search completed: April 12, 2003, 07:16:45
Job time : 5888.03 secs

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Qy 1921 GAGTATCTAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
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RESULT 2
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AC AAAG3876 standard; DNA: 10562 BP.
XX A.A93876;
XX

15-JAN-2001 (first entry)
Human beta3gal-T5 encoding DNA.
Beta-3 galactose transferase; treatment; diagnosis; cancer; human;
digestive system; beta3gal-T5; ds.
Homo sapiens.
KC200050608.A1.
31-AUG-2000.
24-FEB-2000; 200000-JP01070.
25-FEB-1999; 99JP-0047571.
(KYON) KYONA HAKKO KOSYO KK.
Nariematsu H, Ishihiki S, Toyayachi A, Sasaki K;
WPI: 2000-549409/50.
Beta-3 galactose transferase and DNA encoding it, useful for
diagnosis of digestive system cancer.
Claim 31; Page 103-111; 123pp; Japanese.
This invention relates to a polypeptide (1) with beta-1,3 galactose
transferase activity, or variants of (1) comprising amino acid additions,
all or part of which substitutions are included in the invention is DNA encoding
all or part of the polypeptide, or variants of the polypeptide, or cells
transformed by the vectors; a method for the preparation of the
polypeptide by culture of the transformants or by expression in the milk
of the transformed cells; a method for the preparation of the beta-1,3
galactose transferase protein; transfers galactose by beta-1,3
N-acetylglucosamine present in a non-cyclic carbohydrate chain (such as
Glucosyl-beta1-3galactosyl-4GLc) to give Galbeta1-3GlcNAc. The protein and
DNA encoding it are useful for the treatment and diagnosis of cancer of
the digestive system. The present sequence represents a beta3gal-T5
encoding DNA sequence.
Sequence 10562 BP; 2610 A; 2415 C; 2574 G; 2963 T; 0 other:
Query Match 83.94; Score 2329; DB 21; Length 10562:
Blast Local Similarity 100.0%, Pred. NO. 0:
Matches 2329; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
Qy 402 ATGCTTTTCCGAGAGAGAGATGANGATATTTGCTCTTGGTCTGGGGGCTTTGT 461
Db 834 ATGCTTTTCCGAGAGAGATGANGATATTTGCTCTTGGTCTGGGGGCTTTGT 893
Qy 462 TGTATTTTACGATGACATGATTAATCTTTTCAAGAGAGCTCTTTGTACAGAAA 521
Db 894 TGTATTTTACGATGACATGATTAATCTTTTCAAGAGAGCTCTTTGTACAGAAA 934
Qy 522 CAGGAGAGCTTTAAAGTCTCCAGATGACAGCTGACAGCAGACCTCTCTCTGTC 581
Db 895 CAGGAGAGCTTTAAAGTCTCCAGATGACAGCTGACAGCAGACCTCTCTCTGTC 943
Qy 582 CTGCTGTGAGCTATCCACAAACAGTTGCTGAGCGATGGGCACTGGCAGAGCTG 641
Db 841 CTGCTGTGAGCTATCCCAACAAACAGTTGCTGAGCGATGGGCACTGGCAGAGCTG 847
Qy 642 GGGAGAGAGAGATGAG 701
Db 847 GGGAGAGAGAGATGAG 853
Qy 702 AGCAGTGCAGGGAG 761
Db 854 AGCAGTGCAGGGAG 893

09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Schlegel R, Endege WO, Monahan JE;
WPI; 2001-66795/76.
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
Claim 1: Page 10355; 11750pp; English.
The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (AA00010-AB062213) of the specification or its complement, is useful for prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) determining whether prostate cancer has metastasized in a compound;
(g) determining the aggressiveness or indolence of prostate cancer in a patient;
(h) is also useful as a pharmacodynamic or pharmacogenomic marker.
Sequence 422 BP; 176 A; 92 G; 63 G; 91 T; 0 other;
Query Match
Best Local Similarity 100.0%; Pred. No. 1,2e-08; Length 422;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2725 ACTCTTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
DB 181 ACTCTTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 231
RESULT 9
ABV19654
ID ABV19654 standard; cDNA, 215 BP.
AC ABV19654;
XX 13-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 19645.
DE Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX Homo sapiens.
CS W0200160860-A2.
PN W0200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001MO-US05171.
XX 17-FEB-2000; 2000US-183131P.
XX 16-MAR-2000; 2000US-189862P.
XX 25-MAY-2000; 2000US-207454P.
XX 19-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-255281P.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Schlegel R, Endege WO, Monahan JE;
WPI; 2001-66795/76.
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
Claim 1: Page 3211-3212; 11750pp; English.
The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (AA00010-AB062213) of the specification or its complement, is useful for prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) determining whether prostate cancer has metastasized in a compound;
(g) determining the aggressiveness or indolence of prostate cancer in a patient;
(h) is also useful as a pharmacodynamic or pharmacogenomic marker.
Sequence 215 BP; 115 A; 17 C; 18 G; 57 T; 8 other;
Query Match
Best Local Similarity 100.0%; Pred. No. 3,2e-08; Length 215;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2726 CTCCTTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
DB 142 CTCCTTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 191
RESULT 10
ABV49421
ID ABV49421 standard; cDNA, 341 BP.
AC ABV49421;
XX 17-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 49412.
DE Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX Homo sapiens.
CS W0200160860-A2.
PN W0200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001MO-US05171.
XX 17-FEB-2000; 2000US-183131P.
XX 16-MAR-2000; 2000US-189862P.
XX 25-MAY-2000; 2000US-207454P.
XX 19-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
XX 13-DEC-2000; 2000US-255281P.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Schlegel R, Endege WO, Monahan JE;
WPI; 2001-66795/76.
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

for detecting presence of prostate cancer, stage of prostate cancer -
 Claim 1: Page 9653, 11750pp; English.
 The invention relates to an isolated nucleic acid molecule (i) comprising a nucleotide sequence given in Tables 1-9 (SAR00010-AR06221) of the specification or its complement, (i) is useful for:
 (a) assessing whether a patient is afflicted with prostate cancer;
 (b) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
 (c) assessing the efficacy of a therapy for inhibiting prostate cancer;
 (d) selecting a composition for inhibiting prostate cancer in a patient;
 (e) selecting the prostate cell carcinogenic potential of a compound;
 (f) determining whether prostate cancer has metastasized in a patient;
 (g) determining the aggressiveness or incidence of prostate cancer in a patient;
 (h) is also useful as a pharmacodynamic or pharmacogenomic marker.
 Sequence 341 BP; 144 A; 64 C; 54 G; 79 T; 0 other;
 Query Match 1.84; Score 50; DB 23;
 Best Local Similarity 100.0%; Frnd No. 56-08; Indels 0; Gaps 0;
 Matches 50; Conservative 0; Mismatches 0;

QY 2726 CTTCTTAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
 DB 180 CTTCTTAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 229
 RESULT 11
 ID A118530 standard: CNA; 383 BP.
 XX Human polynucleotide SEQ ID NO 8530.
 XX Homo sapiens.
 XX WO200164835-A2.
 XX 07-SEP-2001.
 XX 26-FEB-2001; 2001:US04927.
 XX 28-FEB-2000; 2000US-0515126.
 XX 18-MAY-2000; 2000US-0577409.
 XX (HYPSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-514839/56.
 XX P-PSDB: AA00359.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 XX diagnosing and treating e.g. leukaemia, inflammation and immune
 XX disorders -
 XX Claim 1: SEQ ID NO 8530; 1399pp + sequence listing; English.
 XX The invention relates to human polynucleotides (AA17951-AA19381) and
 XX the encoded proteins (AA00000-AA03910) that exhibit activities as a
 XX cytokine, cell proliferation or cell differentiation or which may induce

Production of other cytokines in other cell populations. The
 peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, hematopoiesis regulating
 activity, inhibits growth factor activity, immunomodulatory activity
 activity, inhibits growth factor activity, immunomodulatory activity
 treatment of cancer, leukaemia, nervous system disorders, arthritis and
 inflammation.
 CC The sequence data for this patent did not form part of the patented
 CC specification, but was obtained from an electron copy of the patent
 CC at ftp.wipo.int/pub/Registered_sequences.
 XX Sequence 383 BP; 192 A; 74 C; 65 G; 52 T; 0 other;
 Query Match 1.84; Score 50; DB 22;
 Best Local Similarity 100.0%; Frnd No. 2.8e-08; Indels 0; Gaps 0;
 Matches 50; Conservative 0; Mismatches 0;

QY 2726 CTTCTTAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
 DB 106 CTTCTTAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 155
 RESULT 12
 ID A1813204 standard: CNA; 386 BP.
 XX Human polynucleotide SEQ ID NO 3264.
 XX Homo sapiens.
 XX WO200164835-A2.
 XX 07-SEP-2001.
 XX 26-FEB-2001; 2001:US04927.
 XX 28-FEB-2000; 2000US-0515126.
 XX 18-MAY-2000; 2000US-0577409.
 XX (HYPSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-514838/56.
 XX P-PSDB: AA003273.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 XX diagnosing and treating e.g. leukaemia, inflammation and immune
 XX disorders -
 XX Claim 1: SEQ ID NO 3264; 1399pp + sequence listing; English.
 XX The invention relates to human polynucleotides (AA17951-AA19381) and
 XX the encoded proteins (AA00000-AA03910) that exhibit activities as a
 XX cytokine, cell proliferation or cell differentiation or which may induce
 XX production of other cytokines in other cell populations. The
 XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
 XX e.g. stem cell growth factor activity, hematopoiesis regulating
 XX activity, tissue growth factor activity, immunomodulatory activity and
 XX activity/inhibin activity and may be useful in the diagnosis and/or
 XX cancer, leukaemia, nervous system disorders, arthritis and
 XX inflammation.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Nipo
 CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 386 BP; 185 A; 46 C; 64 G; 85 T; 6 other: 0;

Query Match 1.84; Score 50; Db 22; Length 386;
 Best Local Similarity 100.0%;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2726 CTTCTTAAAAA..... 2775
 Db 123 CTTCTTAAAAA..... 172

RESULT 33

AI186760

ID AI186760 standard; cDNA: 419 BP.

XX AI186760;

DT 06-NOV-2001 (first entry)

XX Human polynucleotide SEQ ID NO 8820.

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 XX tissue growth factor; immunomodulatory; Cancer: leukemia;
 XX nervous system disorders; arthritis; inflammation; ss.

XX Homo sapiens.

XX MOJ00164935-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001MO-US04927.

XX 28-FEB-2000; 2000US-0515126.

XX 18-MAY-2000; 2000US-0577409.

XX (WYSE-) MYSD INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514938/36.

XX P-FSUS; AB04722.

PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukemia, inflammation and immune
 PT disorders.

PS Claim 1: SEQ ID NO 8820; 1399pp - Sequence Listing: English.

CC The invention relates to human polynucleotides (AI179941-AI193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, immunomodulatory activity and
 CC activity/tissue growth factor activity. Immunomodulatory activity and
 CC activity/inhibit activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC Notes: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from Nipo
 CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 419 BP; 154 A; 102 C; 88 G; 75 T; 0 other;

Query Match 1.84; Score 50; Db 22; Length 419;
 Best Local Similarity 100.0%;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2726 CTTCTTAAAAA..... 2775
 Db 126 CTTCTTAAAAA..... 175

RESULT 14

AI184653

ID AI184653 standard; cDNA: 427 BP.

XX AI184653;

DT 06-NOV-2001 (first entry)

XX Human polynucleotide SEQ ID NO 4713.

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 XX tissue growth factor; immunomodulatory; Cancer: leukemia;
 XX nervous system disorders; arthritis; inflammation; ss.

XX Homo sapiens.

XX MOJ00164935-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001MO-US04927.

XX 28-FEB-2000; 2000US-0515126.

XX 18-MAY-2000; 2000US-0577409.

XX (WYSE-) MYSD INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514938/36.

XX P-FSUS; AB04722.

PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukemia, inflammation and immune
 PT disorders.

PS Claim 1: SEQ ID NO 4713; 1399pp + Sequence Listing: English.

CC The invention relates to human polynucleotides (AI179941-AI193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, immunomodulatory activity and
 CC activity/inhibit activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC Notes: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from Nipo
 CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 427 BP; 170 A; 87 C; 85 G; 83 T; 0 other;

Query Match 1.84; Score 50; Db 22; Length 427;
 Best Local Similarity 100.0%;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2726 CTTCTTAAAAA..... 2775
 Db 137 CTTCTTAAAAA..... 186

RESULT 15

Search completed: April 12, 2003, 03:51:25
Job time : 491.571 secs


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/Note="Vector: pBAK3.6; Site.1: EcoRI; Site.2: EcoRI;
/RC11="Human Male BAC Library"
BASE COUNT      101 a 146 c 104 g 175 t 2 others
ORIG-IN

Query Match      6.5%; Score 181; DB 37; Length 328;
Best Local Similarity 100.0%; Pred. No. 8e-37;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 GAGTCAGAGCTCTCGGCTTGGACGAGGATTATACACAGAGTTTCTGGGTC 120
DB 56 GAGTCAGAGCTCTCGGCTTGGACGAGGATTATACACAGAGTTTCTGGGTC 115
QY 121 TCAAGCTTGGGCTTGAGTATGATATACAGTCGCAATCTGGGTCGAGGCTT 180
DB 116 TCAAGCTTGGGCTTGAGTATGATATACAGTCGCAATCTGGGTCGAGGCTT 175
QY 181 GGTCTTGAGCAACATCTCGATTCAGTCCAGCTCTCGATTCGATCGCTGAC 240
DB 176 GGTCTTGAGCAACATCTCGATTCAGTCCAGCTCTCGATTCGATCGCTGAC 235
QY 241 G 241
DB 236 G 236

RESULT 5
LOCUS      AJ003597.3 338 bp mRNA linear EST 04-DEC-1997
DEFINITION      AJ003597 selected chromosome 21 cDNA library Homo sapiens cDNA
ACCESSION      AJ003597.1 GI:2578270
VERSION        AJ003597.1
KEYWORDS       EST;
SOURCE        Human
ORGANISM      Homo sapiens
REFERENCE      Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
              Hymenoptera: Diptera: Primates: Catarrhini: Hominoidea: Homo.
AUTHORS        Sulzewska J., Hunt E., Nguyen M., Korn B., Rohrdanz B., Lehrach
              J. and Vespö M. L. H.
TITLE          Unpublished cDNA library: Selected cDNA library for the whole human chromosome 21
JOURNAL        Unpublished (1997)
COMMENT        Contact: Vespö, M. L.
              Max Planck Institut fuer Molekulare Genetik
              Im Neuenheimer Feld 287, D-70550 Heidelberg, Germany.
              E-mail: vesp@molgen.mpg.de
              Location/Qualifiers
              source          1. 338
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /map="21q"
              /clone="Mrip9-1229"
              /clone_lib="Selected chromosome 21 cDNA library"
              /notes="Nucleotide coordinates: 87 c, 82 g, 92 c, 76 a"
BASE COUNT      76 a 92 c 82 g 2 others
ORIGIN

Query Match      5.9%; Score 145; DB 9; Length 338;
Best Local Similarity 99.5%; Pred. No. 4.8e-28;
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 439 TTCTGGCTTGGGCTCTGCTTGTATTTAGCATGTACAGTTCAGGTCCTGAG 498
DB 312 TTCTGGCTTGGGCTCTGCTTGTATTTAGCATGTACAGTTCAGGTCCTGAG 253
QY 498 AAGAGCTCTTGTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
DB 252 AAGAGAGCTCTTGTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 193
QY 558 AGCAGAGCTCTTGTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618
DB 192 AGCAGAGCTCTTGTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 133

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QY 619 GATGTGCATCGCGACAGCTGGGGGGAAGAGGA 654
DB 132 GATGTGCATCGCGACAGCTGGGGGGAAGAGGA 97

RESULT 6
LOCUS      BE599666.1 108 bp mRNA linear EST 12-SEP-2000
DEFINITION      BE599666-105-105 UN084 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BE599666.1 GI:10087408
VERSION        BE599666.1
KEYWORDS       EST;
SOURCE        Human
ORGANISM      Homo sapiens
REFERENCE      Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
              Primates: Catarrhini: Hominoidea: Homo.
AUTHORS        Das Neto E., Garcia Correa R., Varjovszky-Almeida S., Brites M. R.,
              Nagai M. Jr., Zago M. A., Bordin S., Costa P. F., D. H.,
              Brunstein A., de Oliveira P. S., Bucher P., Jongeneel C. V., O'Hare
              M. J., Soares F., Brentani R. R., Reis L. F., de Souza S. J. and
              Simpson A. J. G.
TITLE          Sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT        Contact: Simpson A.J.G.
              Ludwig Institute for Cancer Research
              Head Prof. Antonio Frudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              E-mail: asimpson@ludwig.org.br
              This entry was submitted to the Eukaryotic Genome Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?l=424-OM-NN0084-100)
              Seq primer: puc-18 forward
              High quality sequence start: 7
              High quality sequence stop: 108.
FEATURES
source          1. 108 //Qualifiers
              /locus="OM-NN0084"
              /db_xref="taxon:9606"
              /map="21q"
              /note="Organ: nervous normal; Vector: puc18; Site.1: SmaI;
              Site.2: SmaI; A mini-library was made by cloning products
              from a cDNA library prepared from human testis tissue.
              NO. 196.116 - Ludwig Institute for Cancer Research
              profiles into the puc 18 vector. Reverse transcription of
              tissue mRNA and cDNA amplification were performed under
              low stringency conditions."
BASE COUNT      21 a 35 c 27 g 25 t
ORIGIN

Query Match      3.7%; Score 104; DB 12; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.8e-14;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1271 GACTCTGTGCTACGTCAGGCTGACAGTTCGGGGGGAATTCGCGCTGT 1330
DB 108 GACTCTGTGCTACGTCAGGCTGACAGTTCGGGGGGAATTCGCGCTGT 49
QY 1331 CTGAGGAGGAGCCGAGAGGCAATCGGCAAGTTCACATATCC 1374
DB 48 CTGAGGAGGAGCCGAGAGGCAATCGGCAAGTTCACATATCC 5

RESULT 7
C91526

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CG126      171 bp mRNA linear EST 20-APR-1998
LOCUS      Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
DEFINITION dictyosoma cDNA clone SK390, mRNA sequence.
ACCESSION GI:3060892
VERSION    1
KEYWORDS   EST.
SOURCE     Dictyostelium discoideum.
ORGANISM   Dictyostelium
COMMENT    Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE  Morito T., Urushihara, H., Saito T., Ugawa Y., Mizuno, M., Yoshida, M., Williams J., Maeda M., Takeuchi I., Ochiai, R. and Tanaka, K. Developmental cDNA in Dictyostelium discoideum Unpublished (1998)
TITLE      Dictyostelium discoideum SS (H.Urushihara)
AUTHORS    Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennouda-4, Tsukuba, Ibaraki 305-8572, Japan
            Tel.: 81-298-53-6614
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES   Feature List:
            Location/Qualifiers
                /organism="Dictyostelium discoideum"
                /strain="AM4"
                /clone="SK390"
                /cdate="1998"
                /cnum="15b"
                /cdesc="Dictyostelium discoideum SS (H.Urushihara)*"
                /dev_stage="slug"
            ..
            106 a 15 c 1 g 49 t
BANK COUNT 106 a 15 c 1 g 49 t
ORIGIN
Query Match Similarity 100%; Score 55; DB 14; Length 171;
Mismatches 0; Gaps 0; Conservative 0; Identical 0; Indels 0;
Gy 2721 CTAATCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
DB 2721 CTAATCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 169

RESULT 8
BE047732
LOCUS      NCI_COAP_Ern2 Homo sapiens cDNA clone IMAGE:229131 5',
DEFINITION NCI-COAP_Ern2 Homo sapiens cDNA clone IMAGE:229131 5',
ACCESSION BE047732
VERSION    1
KEYWORDS   mRNA sequence.
SOURCE     human.
ORGANISM   Homo sapiens
COMMENT    Bakardira; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Primates; Catarrhini; Hominoidea; Homo.
            1 bases 1 to 267
NCI-COAP http://www.ncbi.nlm.nih.gov/ncicqap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
            National Cancer Institute, Biotechnology Resource Project,
            Transposoncentric, Christopher A. Meskall, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
CDB Library Preparation: Life Technologies, Inc.
Cloning Vector: pCMVcat
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-COAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LIN, send email to:
lin@imagine.jax.org
Seq primer: -40BP from Gibco.
Location/Qualifiers
            1..267
            ..
            106 a 15 c 1 g 49 t
FEATURES   Feature List:
            Location/Qualifiers

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: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 64
: LENGTH: 2301
: TYPE: DNA
: ORGANISM: Brassica napus
US-09-821-994-64

Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-11; Length 2301;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2726 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
|||||.....|
Db 1371 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1420
|||||.....|

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RESULT 3
US-09-232-191-8
: Sequence 8, Application US/09232191
: Patent No. 6284487
: GENERAL INFORMATION:
: APPLICANT: Stahl, Andreas
: APPLICANT: Hirsch, David J.
: APPLICANT: Glemo, Ruth E.
: APPLICANT: Lodish, Harvey F.
: TITLE OF INVENTION: Fatty Acid Transport Proteins
: CURRENT APPLICATION NUMBER: US/09/232.191
: CURRENT FILING DATE: 1999-01-14
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/110,941
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 301
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-191-8

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Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2726 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
|||||.....|
Db 2240 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2289
|||||.....|

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RESULT 4
US-09-232-200-8
: Sequence 8, Application US/09232200A
: Patent No. 6288213
: GENERAL INFORMATION:
: APPLICANT: Stahl, Andreas
: APPLICANT: Hirsch, David J.
: APPLICANT: Glemo, Ruth E.
: APPLICANT: Lodish, Harvey F.
: APPLICANT: Glemo, Ruth E.
: APPLICANT: Lodish, Harvey F.
: TITLE OF INVENTION: Fatty Acid Transport Proteins
: FILE REFERENCE: WH197-21p3M8
: CURRENT APPLICATION NUMBER: US/09/232.200A
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-01-15
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/110,941
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FastSeq for Windows Version 3.0

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: SEQ ID NO 8
: LENGTH: 2301
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-200-8

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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2726 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
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Db 2240 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2289
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RESULT 5
US-09-232-197-8
: Sequence 8, Application US/0923197A
: Patent No. 6284487
: GENERAL INFORMATION:
: APPLICANT: Stahl, Andreas
: APPLICANT: Hirsch, David J.
: APPLICANT: Glemo, Ruth E.
: APPLICANT: Lodish, Harvey F.
: APPLICANT: Tartaglia, Louis A.
: TITLE OF INVENTION: Fatty Acid Transport Proteins
: CURRENT APPLICATION NUMBER: US/09/232.197A
: CURRENT FILING DATE: 1999-01-14
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/110,941
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 301
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-197-8

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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2240 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2289
|||||.....|

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RESULT 6
US-09-232-201-8
: Sequence 8, Application US/09232201A
: Patent No. 6348321
: GENERAL INFORMATION:
: APPLICANT: Stahl, Andreas
: APPLICANT: Hirsch, David J.
: APPLICANT: Glemo, Ruth E.
: APPLICANT: Lodish, Harvey F.
: APPLICANT: Glemo, Ruth E.
: APPLICANT: Lodish, Harvey F.
: TITLE OF INVENTION: Fatty Acid Transport Proteins
: FILE REFERENCE: WH197-21p3M3
: CURRENT APPLICATION NUMBER: US/09/232.201A
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-01-15
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/110,941
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 105

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: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 8
: LENGTH: 2301
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-201-8

Query Match
: Sequence 44, Application US/09232200A
: Patent No. 628813
: Applicant: Stahl, Andreas
: Applicant: Hirsch, David J.
: Applicant: Lodish, Harvey F.
: Applicant: Glimo, Ruch E.
: Applicant: Tartaglia, Louis A.
: TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
: CURRENT APPLICATION NUMBER: US/09/232-200A
: CURRENT FILING DATE: 1999-01-14
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/110,941
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 44
: SEQ ID NO 45
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-200-44

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: Best Local Similarity 100.0%; Pred. No. 2,6e-11;
: Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 2649 CTTCTTAAAAA 100.0%

Query Match
: Sequence 44, Application US/09232200A
: Patent No. 628813
: Applicant: Stahl, Andreas
: Applicant: Hirsch, David J.
: Applicant: Lodish, Harvey F.
: Applicant: Glimo, Ruch E.
: Applicant: Tartaglia, Louis A.
: TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
: CURRENT APPLICATION NUMBER: US/09/232,197A
: CURRENT FILING DATE: 1999-01-14
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/110,941
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 44
: SEQ ID NO 45
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-197-44

Query Match
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: Best Local Similarity 100.0%; Pred. No. 2,6e-11;
: Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2726 CTTCTTAAAAA 100.0%
DB 2649 CTTCTTAAAAA 100.0%

Query Match
: Sequence 70: Application US/09232197A
: Patent No. 6300096
: GENERAL INFORMATION:
: Applicant: Stahl, Andreas
: Applicant: Hirsch, David J.
: Applicant: Lodish, Harvey F.
: Applicant: Glimo, Ruch E.
: Applicant: Tartaglia, Louis A.
: TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
: CURRENT APPLICATION NUMBER: US/09/232,197A
: CURRENT FILING DATE: 1999-01-14
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 44
: SEQ ID NO 45
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-200-70

Query Match
: Sequence 70: Application US/09232197A
: Patent No. 6300096
: GENERAL INFORMATION:
: Applicant: Stahl, Andreas
: Applicant: Hirsch, David J.
: Applicant: Lodish, Harvey F.
: Applicant: Glimo, Ruch E.
: Applicant: Tartaglia, Louis A.
: TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
: CURRENT APPLICATION NUMBER: US/09/232,197A
: CURRENT FILING DATE: 1999-01-14
: EARLIER APPLICATION NUMBER: 60/071,374
: EARLIER FILING DATE: 1998-07-20
: EARLIER APPLICATION NUMBER: 60/093,491
: EARLIER FILING DATE: 1998-12-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 44
: SEQ ID NO 45
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-232-200-70

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; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FASTSEQ for Windows Version 3.0
; LENGTH: 2710
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-232-201-70

Query Match
Local Similarity 100.0% DB 4: Length 2710;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2726 CTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
DB 2649 CTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2698

RESULT 11
US-09-232-201-44
; Sequence 44, Application US/0923201A
; Patent No. 6348321
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; REFERENCE: WH197-2P3MC US/09/232,201A
; CURRENT FILING DATE: 1999-01-16
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 2710
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-232-201-44

Query Match
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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2649 CTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2698

RESULT 12
US-09-232-201-70
; Sequence 50, Application US/0923201A
; Patent No. 6348321
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; REFERENCE: WH197-2P3MC US/09/232,201A
; CURRENT APPLICATION NUMBER: US/09/232,201A
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-16
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; NUMBER OF SEQ ID NOS: 105
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; SEQ ID NO 50
; LENGTH: 2710
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-232-201-70

Query Match
Local Similarity 100.0% DB 4: Length 2710;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2649 CTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2698

RESULT 13
US-09-410-464-14
; Sequence 14, Application US/09410464
; Patent No. 6395892
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE OF INVENTION: poplar and other plant species.
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1998-04-04
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE:
; SEQ ID NO 14
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; NAME/KEY: CDS
; FEATURE:
; CDS: (95)..(815)
US-09-410-464-14

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Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-08-553-367A-5
; Sequence 5, Application US/08553367A
; Patent No. 5939539
; APPLICANT: Theodor Lange et al.
; TITLE OF INVENTION: CA 30-OXIDASE GENE SEQUENCES (As Amended)
; NUMBER OF SEQUENCES: 19
; REFERENCE: US/08/553,367A
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: U.S.A.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER FILE NAME: US-08-553-367A-5
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS

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SOFTWARE: Wordperfect 5.1
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FILING DATE: No. 59395September 27, 1995
CLASSIFICATION: 800
PAGES IN CURRENT DATA:
APPLICATION NUMBER:
FILING DATE:
NAMES/AGENTS INFORMATION:
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 49/FD-5M2
ATTORNEY NAME AND FIRM INFORMATION:
TELEPHONE: 303-721-8200
TELEFAX: 203-721-8250
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: nucleotide base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
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Best Local Similarity 100.0%; Pred No. 7e-11;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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05-295-306-5 Application US/0295306
Serial Number: 5, 6198021mer 27, 1995
Patent No. 6198021mer 27, 1995
GENERAL INFORMATION:
APPLICANT: THEODOR LANGE et al.
INVENTOR: THEODOR LANGE et al.
NUMBER OF SEQUENCES: 15
SEQUENCE LENGTH: 1000-2000 NUCLEOTIDES
CORRESPONDENCE ADDRESS:
DR. THEODOR LANGE, Institut fuer Genetik,
Ammersee 203, Wendguth, Lind & Ponank, L.U.P.
c/o Dr. Theodor Lange, D-30559, Hildesheim,
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microperfect 5.1
COMMENTS: ALL INFORMATION IS DATA
APPLICATION NUMBER: US/09/295, 306
CLASSIFICATION:
FILING DATE:
PUBLICATION DATE:
PRIORITY APPLICATION NUMBER: 08/553,367
FILING DATE: NO. 6198021mer 27, 1995
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 45/DIV-FD4 5M2
TELEPHONE: 202-721-6800
FACSIMILE: 202-721-6800

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Run on: April 12, 2003, 08:22:00 ; Search time 177.677 Seconds
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Title: US-09-914-152-2

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11

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post-processing: Listing first 45 summaries

Database : Published Applications NA-1-

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7	50	1.8	1939	9	US-10-067-761-4	Sequence 4, App
8	50	1.8	1939	9	US-10-067-761-4	Sequence 4, App
9	50	1.8	1939	10	US-09-84-136-4	Sequence 2, App
10	50	1.8	1939	10	US-09-84-136-4	Sequence 2, App
11	50	1.8	2371	9	US-09-35-63-2	Sequence 9, App
12	50	1.8	2371	9	US-09-35-63-2	Sequence 9, App
13	49	1.8	86	9	US-09-768-627-39	Sequence 9, App
14	49	1.8	86	9	US-09-768-627-39	Sequence 9, App
15	49	1.8	370	10	US-09-96-102-332	Sequence 332, App
16	49	1.8	370	10	US-09-96-102-332	Sequence 332, App
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22	49	1.8	1159	9	US-10-104-860-14	Sequence 545, App
23	49	1.8	1166	10	US-09-935-101-545	Sequence 104, App
24	49	1.8	1166	10	US-09-935-101-545	Sequence 104, App
25	49	1.8	1434	9	US-10-097-883-103	Sequence 104, App
26	49	1.8	1434	9	US-10-097-883-103	Sequence 104, App
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20	49	1	1866	9	US-10-0931-683-29	Sequence 29, Appl
21	49	1	1456	10	US-09-764-846-29	Sequence 29, Appl
22	49	1	1459	9	US-10-114-993-70	Sequence 70, Appl
23	49	1	1459	9	US-10-114-993-70	Sequence 70, Appl
24	49	1	1735	10	US-09-764-853-200	Sequence 200, App
25	49	1	1766	9	US-10-142-835-27	Sequence 27, Appl
26	49	1	2379	9	US-10-078-70-133	Sequence 133, App
27	49	1	2379	9	US-10-078-70-133	Sequence 133, App
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43	49	1	3845	9	US-10-142-835-207	Sequence 207, App
44	49	1	3845	9	US-10-144-735-207	Sequence 207, App
45	49	1	6035	10	US-09-680-728-35	Sequence 35, Appl

ALIGNMENTS

```

RESULT 1
US-09-739-234-21
Sequence 21, Application US/09739254
Patent No. US20020624041
GENERAL INFORMATION: 48 Human Secreted Proteins
APPLICANT: Rosen et al.
TITLE OF INVENTION: 48 Human Secreted Proteins
CURRENT FILING DATE: 2000-12-19
CURRENT APPLICATION NUMBER: US/09/739,254
EARLIER APPLICATION NUMBER: 00/511,554
EARLIER FILING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: PCT/US99/19310
EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/097,917
EARLIER FILING DATE: 1998-06-25
EARLIER APPLICATION NUMBER: 08/050,694
EARLIER FILING DATE: 1998-06-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 1
LENGTH: 1443
TYPE: DNA
ORGANISM: Homo sapiens
US-09-739-234-21
Query Match
Best Local Similarity : 1.8%; Score 50; DB: 1443;
Watches 50; Conservative 0; Mismatches 0; Indels 0
YD 2736 CTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
DB 1397 CTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1436
RESULT 2
US-09-904-615-21
Sequence 21, Application US/09904615
Patent No. US20020624041
GENERAL INFORMATION: 48 Human Secreted Proteins
TITLE OF INVENTION: 48 Human Secreted Proteins

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1 PRIOR FILING DATE: 1995-09-09
2 PRIOR APPLICATION NUMBER: 60/162,979
3 PRIOR FILING DATE: 1995-11-01
4 PUBLICATION NO.: 5,952,719
5 SOFTWARE: PatentIn Ver. 2.0
6 SEQ ID NO 2
7 LENGTH: 1939
8 ORGANISM: Homo sapiens
9 FEATURE:
10 NAME/KEY: SITE
11 LOCATION: 138
12 OTHER INFORMATION: n equals a.t.g. or c
13 FEATURE:
14 NAME/KEY: SITE
15 LOCATION: 138
16 OTHER INFORMATION: n equals a.t.g. or c
17 FEATURE:
18 NAME/KEY: SITE
19 LOCATION: 138
20 OTHER INFORMATION: n equals a.t.g. or c
21 US-10-125-459-2
22 Query Match 1.8% Score 50: Db 9: Length 1939;
23 Best Local Similarity 100.0%: Pred No. 26-15; Mismatches 0; Indels 0; Gaps 0:
24 Oy 2726 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
25 db 1853 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1902
26 RESULT 5
27 US-10-67-761-4
28 Sequence 4 Application US/10057761
29 Publication No. US20020197701A1
30 GENERAL INFORMATION:
31 TITLE OF INVENTION: Serine protease polynucleotides, Polypeptides, and Antic
32 FILE OF REFERENCE: P70054
33 CURRENT APPLICATION NUMBER: US10/067,761
34 PUBLICATION NUMBER: 5,952,719
35 PRIOR APPLICATION NUMBER: 09/849,156
36 PRIOR FILING DATE: 2001-03-13
37 PRIOR APPLICATION NUMBER: 60/189,025
38 PUBLICATION NUMBER: 5,952,719
39 NUMBER OF SEQ ID NOS: 3
40 SOFTWARE: PatentIn Ver. 2.0
41 SEQ ID NO 4
42 LENGTH: 1939
43 TYPE: DNA
44 ORGANISM: Homo sapiens
45 FEATURE:
46 NAME/KEY: SITE
47 LOCATION: 138
48 OTHER INFORMATION: n equals a.t.g. or c
49 FEATURE:
50 NAME/KEY: SITE
51 LOCATION: 138
52 OTHER INFORMATION: n equals a.t.g. or c
53 US-10-067-761-4
54 Query Match 1.8% Score 50: Db 9: Length 1939;
55 Best Local Similarity 100.0%: Pred No. 26-15; Mismatches 0; Indels 0; Gaps 0:
56 Oy 2726 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
57 db 1853 CTTCTTAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1902

```



```

RESULT 6
US-09-804-156-4
: Sequence 4, Application US/09804156
: BEST LOCAL SIMILARITY 100.0%, Pred. No. 2e-15, Mismatches 0; Gaps 0;
: GENERAL INFORMATION
: ORGANISM: Homo sapiens
: APPLICANT: Shi, et al.
: TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
: CURRENT APPLICATION NUMBER: US/09/804.156
: CURRENT FILING DATE: 2001-03-13
: PRIOR APPLICATION NUMBER: 60/189,025
: PRIOR FILING DATE: 2000-03-14
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 1939
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: SITE
: LOCATION: (308)
: OTHER INFORMATION: n equals a.t.g. or c
: NAME/KEY: SITE
: LOCATION: (1938)
: OTHER INFORMATION: n equals a.t.g. or c
: NAME/KEY: SITE
: LOCATION: (1938)
: OTHER INFORMATION: n equals a.t.g. or c
US-09-804-156-4
: Query Match
: Best Local Similarity 100.0%, Pred. No. 2e-15, Mismatches 0; Gaps 0;
: Matches 50; Conservative 0; Mismatches 15; 0; Indels 0;
Qy 2726 CTTCTTAAAAA 184; Score 50; DB 10; Length 1939;
Db 1853 CTTCTTAAAAA 100.0%; Pred. No. 2e-15; Mismatches 0; Indels 0; Gaps 0;

US-09-946-633-2
: Sequence 2, Application US/0946633
: BEST LOCAL SIMILARITY 100.0%, Pred. No. 2e-15, Mismatches 0; Gaps 0;
: GENERAL INFORMATION
: ORGANISM: Homo sapiens
: APPLICANT: Ni, et al.
: TITLE OF INVENTION: PT005P1
: CURRENT APPLICATION NUMBER: US/09/946.633
: CURRENT FILING DATE: 2001-09-06
: PRIOR APPLICATION NUMBER: 09/597,839
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/133,239
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/135,163
: PRIOR FILING DATE: 1999-08-03
: PRIOR APPLICATION NUMBER: 60/147,005
: PRIOR FILING DATE: 1999-08-03
: PRIOR APPLICATION NUMBER: 60/152,935
: PRIOR FILING DATE: 1999-11-01
: PRIOR APPLICATION NUMBER: 60/162,979
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1939
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: SITE
: LOCATION: (1915)
: OTHER INFORMATION: n equals a.t.g. or c
: NAME/KEY: SITE
: LOCATION: (1915)

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: OTHER INFORMATION: n equals a.t.g. or c
: NAME/KEY: SITE
: LOCATION: (1938)
: OTHER INFORMATION: n equals a.t.g. or c
US-09-946-633-2
: Query Match
: Best Local Similarity 100.0%, Pred. No. 2e-15, Mismatches 0; Gaps 0;
: Matches 50; Conservative 0; Mismatches 0; Indels 0;
Qy 2726 CTTCTTAAAAA 184; Score 50; DB 10; Length 1939;
Db 1853 CTTCTTAAAAA 100.0%; Pred. No. 2e-15; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-09-943-671-8
: Sequence 8, Application US/09943671
: BEST LOCAL SIMILARITY 100.0%, Pred. No. 2e-15, Mismatches 0; Gaps 0;
: GENERAL INFORMATION
: ORGANISM: Mus musculus
: APPLICANT: Blirsch, David J.
: TITLE OF INVENTION: Fatty Acid Transport Proteins
: CURRENT APPLICATION NUMBER: US/09/943.671
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/232,191
: PRIOR FILING DATE: 1998-07-20
: PRIOR APPLICATION NUMBER: 60/091,491
: PRIOR FILING DATE: 1998-07-20
: PRIOR APPLICATION NUMBER: 60/110,941
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 9301
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-943-671-8
: Query Match
: Best Local Similarity 100.0%, Pred. No. 2e-15, Mismatches 0; Gaps 0;
: Matches 50; Conservative 0; Mismatches 0; Indels 0;
Qy 2726 CTTCTTAAAAA 184; Score 50; DB 10; Length 2301;
Db 2240 CTTCTTAAAAA 100.0%; Pred. No. 2e-15; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-968-827-39
: Sequence 39, Application US/09768827
: BEST LOCAL SIMILARITY 100.0%, Pred. No. 2e-15, Mismatches 0; Gaps 0;
: GENERAL INFORMATION
: ORGANISM: Homo sapiens
: APPLICANT: Schaefer, Robert
: TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, PREVENTION, AND THERAPY OF HUMAN PROSTATE CANCER
: CURRENT APPLICATION NUMBER: US/09/968.827
: CURRENT FILING DATE: 2000-01-24
: PRIOR APPLICATION NUMBER: US 60/178,525
: PRIOR FILING DATE: 2000-01-24
: PRIOR APPLICATION NUMBER: US 60/183,245
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: US 60/190,139
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: US 60/208,126
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: US 60/219,705

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Query Match      1.8% Score 49: DA 10: Length 370:
Best Local Similarity 100.0%: Pred. No. 6.7e+15:
Matches 49: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2129 TCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2775
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DD 233 TCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 281

RESULT 11
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: Sequence 332, Application US/10091504
: Publication No. US20030295908a1
: GENERAL INFORMATION:
:   TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
:   FILE REFERENCE: EC007C1
:   CURRENT PUBLICATION NUMBER: US/410/091_504
:   CURRENT FILING DATE: 03-07
:   NUMBER OF SEQ ID NOS: 2442
: Prior Application removed - See File Wrapper or Paim
:   SEQ ID NO: 1, Protein Ver. 2.0
:   SEQ ID NO 32
:   LENGTH: 439
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURES:

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[illegible]

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1  CURRENT APPLICATION NUMBER: US/09/770.444
2  CURRENT FILING DATE: 2001-01-26
3  PRIOR APPLICATION NUMBER: 60/178.502
4  PRIOR FILING DATE: 2000-01-27
5  SOFTWARE: FastSeq for Windows Version 4.0
6  SEQ ID NO 872
7  LENGTH: 442
8  ORIGIN: Arabidopsis thaliana
9  US-09-770-444-872

10 Query Match
11     1.8% Score 49; DB 10; Length 442;
12     Best Local Similarity 100.0%; Pred. No. 6.7e-15;
13     Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
14
15 QY 2727 TCTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2775
16     |||||
17 DB 67 TCTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 19

18 RESULT 14
19 US-104-580-14
20     1.8% Score 49; DB 10; Length 442;
21     Best Local Similarity 100.0%; Pred. No. 6.7e-15;
22     Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23
24 QY 2727 TCTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2775
25     |||||
26 DB 67 TCTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 19

27 RESULT 15
28 US-09-925-301-545
29     1.8% Score 49; DB 10; Length 1176;
30     Best Local Similarity 100.0%; Pred. No. 6.6e-15;
31     Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
32
33 QY 2727 TCTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2775
34     |||||
35 DB 1127 TCTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1175

36 Search completed, April 12, 2003, 12:47:52
37 Job time : 213.677 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK Nucleic - nucleic search, using sw model
Run on: April 11, 2003, 14:22:18 ; Search time 1364.65 Seconds
15994.713 Million cell updates/sec
Title: US-09-914-152-3_COPY_1_750
Perfect score: 701
Sequence: 1 ccctctgcgcgaagtagcc.....ctagaatagaagtagattcct 750
Scoring table: IGENITY.MWC
Gapop 10.0.0. Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 100
Listing first 45 summaries

Database : GenBank:
1: gb-ba:
2: gb-ba:
3: gb-ba:
4: gb-ba:
5: gb-ba:
6: gb-ba:
7: gb-ba:
8: gb-pl:
9: gb-pr:
10: gb-pr:
11: gb-st:
12: gb-st:
13: gb-un:
14: gb-un:
15: gb-un:
16: em-fun:
17: em-fun:
18: em-fun:
19: em-fun:
20: em-fun:
21: em-or:
22: em-or:
23: em-pat:
24: em-ph:
25: em-ph:
26: em-ph:
27: em-st:
28: em-un:
29: em-un:
30: em-un:
31: em-un:
32: em-un:
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36: em-un:
37: em-un:
38: em-un:
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44: em-un:
45: em-un:

score greater than or equal to the score of the result being printed,
and is derived by dividing the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750	100.0	170131	9	E8420 Novel poly
2	750	100.0	170131	9	E8420 Novel poly
3	750	100.0	340000	9	HS120380 Homo sapi
4	493.2	54.4	185982	2	AC072321 Homo sapi
5	493.2	54.4	185982	2	AC072321 Homo sapi
6	61.6	18.2	22295	9	AC070868 Homo sapi
7	57.8	7.7	162063	9	AC015553 Homo sapi
8	57.8	7.7	162063	9	AC015553 Homo sapi
9	57.8	7.7	175932	9	AL157894 Homo sapi
10	56.6	7.5	173959	2	AP009922 Homo sapi
11	55.4	7.4	68444	2	AC114686 Homo sapi
12	55.4	7.4	68444	2	AC114686 Homo sapi
13	55.4	7.4	68444	2	AC114686 Homo sapi
14	55.2	7.4	159555	9	AC007374 Homo sapi
15	55	7.3	207558	2	AC114778 Homo sapi
16	54.4	7.3	157402	2	AC034151 Homo sapi
17	54.4	7.3	157402	2	AC034151 Homo sapi
18	54	7.2	197760	2	AC016466 Homo sapi
19	53.8	7.2	119944	9	AC011162 Homo sapi
20	53.8	7.2	159723	2	AC021862 Homo sapi
21	53.8	7.2	159723	2	AC021862 Homo sapi
22	53.8	7.2	159723	2	AC021862 Homo sapi
23	53.6	7.1	71334	6	AX347027 Sequence
24	53.6	7.1	71334	6	AX347027 Sequence
25	53.6	7.1	71334	6	AX347027 Sequence
26	53.4	7.1	124521	3	DM011594 Homo sapi
27	53.4	7.1	6593	9	AL511367 Human DNA
28	53.4	7.1	19517	3	DM037511 Homo sapi
29	53.4	7.1	19517	3	DM037511 Homo sapi
30	53.4	7.1	201156	9	AL311383 Human DNA
31	53	7.1	21760	9	AL450331 Human DNA
32	52.8	7.0	163903	9	AC007387 Homo sapi
33	52.8	7.0	163903	9	AC007387 Homo sapi
34	52.8	7.0	214523	9	AC005844 Homo sapi
35	52.6	7.0	144201	9	AC112213 Homo sapi
36	52.6	7.0	174293	9	AC113169 Homo sapi
37	52.4	7.0	178905	9	AC007116 Homo sapi
38	52.4	7.0	192239	9	AC009796 Homo sapi
39	52.4	7.0	204140	9	AC010976 Homo sapi
40	52.4	7.0	204140	9	AC010976 Homo sapi
41	52.4	7.0	215973	2	AC009802 Homo sapi
42	52.4	7.0	215973	2	AC009802 Homo sapi
43	52.2	7.0	39163	9	HSS75416 Homo sapi
44	52.2	7.0	113639	9	HS744A17 Homo sapi
45	52.2	7.0	158661	9	HS4271736 Homo sapi

ALIGNMENTS

RESULT 1	E8420	Novel polypeptide.	10562 bp	DNA	linear	PAT 31-JAN-2002
DEFINITION	E8420	Novel polypeptide.				
ACCESSION	E8420	GI:1626994				
VERSION	E8420.1	GI:1626994.1				
ORGANISM	E8420	Homo sapiens				
SOURCE	E8420	Homo sapiens				
REFERENCE	E8420	Homo sapiens				
AUTHORS	E8420	Homo sapiens				
TITLE	E8420	Homo sapiens				
JOURNAL	E8420	Homo sapiens				

Patent. JP 200245464-A 2 12-SEP-2000;

[illegible]


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/db_xref="taxon:9606"
/clone="F081-7294"
1. 1724
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828..10160
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60625..69050
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69158..78529
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145670..164596
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misc_feature
164597..22405
/note="assembly_name:Contig27"
BASE COUNT 53704 a 39120 c 39561 g 51192 t 2405 others
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18 00: Score 135; DB 2; Length 185982;
Query Match 95.34; Pred. No. 5e-21;
Matches 146; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGCTTCGCGACGTAGACCTCTGAGCGCAACTGAGTGTGGTGTGTAGACGGAAT 60
DB 6185 CGCTTCGCGACGTAGACCTCTGAGCGCAACTGAGTGTGGTGTGTAGACGGAAT 6126
QY 61 ATATCTGCTGGCATGACGACCTCTGAGCGCAACTGAGTGTGGTGTGTAGACGGAAT 120
DB 6125 ATATCTGCTGGCATGACGACCTCTGAGCGCAACTGAGTGTGGTGTGTAGACGGAAT 6166

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QY 121 AGTTTGCCACAGGCGACAGGTGTAGA 147
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DB 6065 AGTTTGCCACAGGCGACAGGTGTAGA 6040

RESULT 6
AC007088
DEFINITION Homo sapiens PAC clone RP6-39421 from Aq33, complete sequence.
ACCESSION AC007088
VERSION AC007088.1 GI:5757556
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eumammalia; Placentalia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22295)
Sullivan J.E. and Waterston, R.
Genomic and complete human genome sequence
Genome Res. 8 (11): 4097-4108 (1998).
9963792
9847074
PUBMED
AUTHORS
Hollman, A., Kelderman, P. and Le, T.
The sequence of homo sapiens PAC clone RP6-39421
Unpublished to 22295)
Waterston, R.H.
Direct Submission
TITLE
Submitted (15-MAR-1999) Genome Sequencing Center, Washington
JOURNAL
MO 63106, USA
4 (bases 1 to 22295)
Waterston, R.H.
Direct Submission
Submitted (21-AUG-1999) Genome Sequencing Center, Washington
JOURNAL
MO 63106, USA
5
Waterston, R. to 22295)
Direct Submission
AUTHORS
Genome Center
Center: Washington University Genome Sequencing Center
Web site: http://genome.wustl.edu/gsc
Contact: sapient@wustl.edu
----- Summary Statistics -----
----- Project name: R_0A039H21 -----

NOTICE: This sequence may not represent the entire insert of this
clone. It may contain one or more overlapping clones.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
40). An attempt was made to resolve all sequencing problems, such
as overlapping reads, by sequencing the overlapping sequence
from more than one subclone, and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
This sequence was generated from part of bacterial clone contigs of
human chromosome X, constructed by the Chromosome X mapping group
at the Sanger Centre, Wellcome Trust Genome Campus, Hinxton, UK.
http://www.sanger.ac.uk/Map/CHUX/

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Db 36991 CATACCTCATGAGGAGGAGCAATTCAT 37021
RESULT 10
LOCUS 12422/c
DEFINITION Homo sapiens chromosome 11 clone RP11-750P5 map 11q22, WORKING
ACCESSION DRAFT SEQUENCE, 35 unordered pieces.
VERSION AP000422.2 GI:8119063
KEYWORDS HTO; HTOCS-PHASE1; HTOCS-RAPIT.
SOURCE Homo sapiens DNA, clone:RP11-750P5.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 173359)
   Fujiyama, A., Yada, T., Totoki, Y., Toyoda, A., Taylor, T. D., Hong-Seon P.,
   Hattori, M., Ishii, K., Matsuda, Y., Nakamura, H., and Sakaki, Y.,
   Homo sapiens 173,359 genomic DNA of 11q22
   Published only in database (1999)
2.
   Hattori, M., Ishii, K., Matsuda, Y., Nakamura, H., and Sakaki, Y.,
   Homo sapiens 173,359 genomic DNA of 11q22
   Published only in database (1999)
3.
   Fujiyama, A., Yada, T., Totoki, Y., Toyoda, A., Taylor, T. D., Hong-Seon P.,
   Hattori, M., Ishii, K., Matsuda, Y., Nakamura, H., and Sakaki, Y.,
   Direct Submission 1999, Mashima Hattori, The Institute of Physical
   and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
   Tsukuba Univ., 1-1-1 Katsushika, Sagamihara, Kanagawa 228-8555,
   Japan (E-mail: hattori@gsc.riken.go.jp; Tel:81-42-778-9933,
   Fax:81-42-778-9924; riken.go.jp; Tel:81-42-778-9933).
   On May 31, 2000 this sequence version replaced g1:6997738.
COMMENT
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Center name: Genomic Center
Center code: RIKEN
Center address: Genomic Sciences Center (GSC)
Web site: http://hgp-gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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Center project name: HmapDraF11
Center clone name: RP11-750P5
-----
Scanning Summary Statistics
Strategy: Dye-terminator ET-amessha; 100% of reads
Assembly program: Phrap; Version 0.990139
Consensus quality: 16259 bases at least Q40
Consensus quality: 16259 bases at least Q20
Consensus quality: 16278 bases at least Q20
Insert size: 16959; sum-of-contigs
Quality coverage: 4.0x in Q20 bases; sum-of-contigs
NOTE: This is a 'working draft' sequence. It currently consists of
35 contigs. The true order of the pieces is not known and their
order in the sequence record is arbitrary. Gaps between the gaps
contigs are represented by Ns. This record will be updated with the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
15727 contig of 15727 bp in length
15728 27186 contig of 11359 bp in length
27287 37387 contig of 10101 bp in length
47388 55912 contig of 8604 bp in length
56993 63632 contig of 7540 bp in length
57333 72241 contig of 9509 bp in length
80760 89061 contig of 8102 bp in length
89162 94975 contig of 5814 bp in length
100459 100459 contig of 5281 bp in length
10604 111824 contig of 5421 bp in length
111825 111958 contig of 5674 bp in length
123074 123074 contig of 6075 bp in length
123075 123075 contig of 6075 bp in length
123076 123076 contig of 6075 bp in length
123122 134542 contig of 6421 bp in length

```


* 91943 92042: gap of unknown length
* 92043 206281: contig of 114239 bp in length
* 206282 206381: gap of unknown length
* 206382 206383: contig of 1177 bp in length.
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Source Location/Qualifiers

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/organism="Homo sapiens"
/chromosome="X"
/map_location="X:9506"
/clone="RP11-51605"
misc_feature
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/clone="RP11-51605"
/chromosome="X"
misc_feature
17165..60411
/clone="RP11-51605"
/assembly_name="Contig12"
vector_side:right"
17165..60411
/clone="RP11-51605"
/assembly_name="Contig14"
misc_feature
60512..91942
vector_side:left"
60512..91942
/clone="RP11-51605"
/assembly_name="Contig13"
misc_feature
92043..206281
/note="Assembly name: Contig15"
misc_feature
206382..207558
/note="Assembly name: Contig15"
/map_location="X:9506"
BASE COUNT 63196 a 51834 c 39615 g 62513 t 400 others
ORIGIN

Query Match 7 34: Score 55; D8 2; Length 207558;
Best Local Similarity 68.5%; Pred. No. 0.0061;
Matches 76; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Qy 638 GTACATTTCTCTACTGATGAGTGTGCAATCTCGTACTGCTGCTCAATGAGCTTTTAC 697
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110423 GTGTATTTTACATGAGGAAAGTAAACATATTTTAAATATATATCTCAACAAATTTTAC 110482
Oy 698 ATATATTTCTGACCCAGTATGACCCAGGCTGAGATGATGAGATGATGATTC 748
|| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110483 ATATGTCACACCCAGTATGACCCAGGCTGAGATGATGAGATGATGATTC 110533
Search completed: April 11, 2003, 20:44:46
Job time : 2556.65 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Computer Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 14:50:38 - Search time 124.03 Seconds
1552.085 Million cell updates/sec

Title score: US-09-914-152-3_COPY_1_750
Sequence: 1 cgcctcgcagagtagacc.....ctagatgaagatgattcgt 750

Scoring table: IDENTITY.MC, Gapex 1.0

Searched: 218239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

- Database: 1: Geneseq_101002.*
- 1: /S1S2/gcgdata/geneseq/emb1/NA1980.DAT.*
 - 2: /S1S2/gcgdata/geneseq/emb1/NA1981.DAT.*
 - 3: /S1S2/gcgdata/geneseq/emb1/NA1982.DAT.*
 - 4: /S1S2/gcgdata/geneseq/emb1/NA1983.DAT.*
 - 5: /S1S2/gcgdata/geneseq/emb1/NA1984.DAT.*
 - 6: /S1S2/gcgdata/geneseq/emb1/NA1985.DAT.*
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 - 9: /S1S2/gcgdata/geneseq/emb1/NA1988.DAT.*
 - 10: /S1S2/gcgdata/geneseq/emb1/NA1989.DAT.*
 - 11: /S1S2/gcgdata/geneseq/emb1/NA1990.DAT.*
 - 12: /S1S2/gcgdata/geneseq/emb1/NA1991.DAT.*
 - 13: /S1S2/gcgdata/geneseq/emb1/NA1992.DAT.*
 - 14: /S1S2/gcgdata/geneseq/emb1/NA1993.DAT.*
 - 15: /S1S2/gcgdata/geneseq/emb1/NA1994.DAT.*
 - 16: /S1S2/gcgdata/geneseq/emb1/NA1995.DAT.*
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 - 18: /S1S2/gcgdata/geneseq/emb1/NA1997.DAT.*
 - 19: /S1S2/gcgdata/geneseq/emb1/NA1998.DAT.*
 - 20: /S1S2/gcgdata/geneseq/emb1/NA1999.DAT.*
 - 21: /S1S2/gcgdata/geneseq/emb1/NA2000.DAT.*
 - 22: /S1S2/gcgdata/geneseq/emb1/NA2001.DAT.*
 - 23: /S1S2/gcgdata/geneseq/emb1/NA2002.DAT.*
 - 24: /S1S2/gcgdata/geneseq/emb1/NA2002.DAT.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	ID	Description
1	750	100-0	10562	21	AAA93876
2	121	161	807	20	Human beta3gal-T5
3	53	6	71	20	Human gene express
4	53	6	71	20	Chemically treated
5	52	4	7	20	Human beta3gal-T5
6	52	4	7	20	Human beta3gal-T5
7	42	4	7	20	Human beta3gal-T5
8	45	6	71	20	Human beta3gal-T5
9	45	6	71	20	Human beta3gal-T5

Human breast cancer	10	45	6	6	1	809	22	AA120997
Genomic sequence	11	45	6	6	1	3619	22	AAK39742
Human digestive system	12	45	4	6	1	3619	22	AAK90083
Human digestive system	13	45	4	6	1	45546	20	AAK23520
Human fetal liver	14	44	5	9	600	22	AAK62810	
Human brain expres	15	44	5	9	600	22	AAK10104	
Human brain expres	16	44	5	9	600	22	AAK11220	
Human bone marrow	17	44	5	9	600	22	AAK17018	
Probe #7797 for ge	18	44	5	9	600	22	AAK17864	
Probe #7797 for ge	19	44	5	9	600	22	AAK17864	
Gene #1523 used to	20	43	8	5	12593	24	AAK55554	
Human prostate exp	21	43	2	5	581	23	AAK51286	
Human fetal liver	22	42	8	5	582	22	AAK63119	
Human brain expres	23	42	8	5	582	22	AAK63119	
Human brain expres	24	42	8	5	582	22	AAK11547	
Human bone marrow	25	42	8	5	582	22	AAK37319	
Probe #1081 for ge	26	42	8	5	582	22	AAK18150	
Human genome-deriv	27	42	8	5	582	24	AAK51112	
Human secreted pro	28	42	8	5	582	24	AAK51112	
Human 5' EST isola	29	42	6	5	459	21	AAK22864	
Human kidney amino	30	42	6	5	459	21	AAK22864	
cDNA encoding nove	32	42	6	5	459	24	AAK81640	
Human immune/huesia	33	42	6	5	7	25837	22	AAK85952
Human kidney amino	34	42	6	5	7	14708	24	AAK58357
Human prostate exp	36	41	6	5	5	456	23	AAK55578
Genomic sequence	37	41	4	5	5	290	22	AAK28563
Human reproductive	38	41	4	5	5	14287	22	AAK28563
Human cardiovascular	39	41	2	5	5	1402	22	AAK36774
Human cardiovascular	40	41	2	5	5	1402	22	AAK36774
Human cardiovascular	41	41	2	5	5	1402	22	AAK36774
Human cardiovascular	42	41	2	5	5	24359	22	AAK56568
Human immune/huesia	43	41	5	5	215	22	AAK59024	
Human polynucleoti	44	41	5	5	445	22	AAK59024	
Human polynucleoti	45	41	5	5	445	22	AAK59024	

ALIGNMENTS

RESULT 1	Human beta3gal-T5 encoding DNA.
AAA53876	Beta-1,3 galactose transferase; treatment; diagnosis; cancer; human digestive system; beta3gal-T5; ds.
ID AAA53876 standard; DNA; 10552 bp.	
XX	15-JAN-2001 (first entry)
XX	
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ALIGNMENTS

RESULT 1
ID AAA93876
ID AAA93876 standard; DNA: 10562 BP.
AC AAA93876;
XX 15-JAN-2001 (first entry)
UT Human beta3gal-T5 encoding DNA.
DE Human beta3gal-T5 encoding DNA.
XX Beta-1,3 galactose transferase; treatment; diagnosis; cancer; human;
XX Digestive system; DNA encoding T5; ds.
OS Homo sapiens.
PK M2020005608.A1.
PK 31-AUG-2000.
PK 24-FEB-2000; 2000NC-JP01070.
XX 25-FEB-1999; 95JP-004751.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Nariatsu H, Ishiki S, Togayachi A, Sasaki K;
XX WPI. 2000-5494/950.
XX Beta-1,3 galactose transferase and DNA encoding it; useful for
XX synthesis of type I staly; Lewis, a carbohydrate for treatment of
XX digestive system cancer.

XX	DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35277.	PR	14-SEP-2000;	2000US-0231055
XX	XX	Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;	PR	21-SEP-2000;	2000US-0231251
XX	KW	Cytostatic; gene therapy; vaccine; metadiazol; ob-	PR	21-SEP-2000;	2000US-0231424
XX	XX		PR	25-SEP-2000;	2000US-0231497
XX	OS	Homo sapiens.	PR	26-SEP-2000;	2000US-0231484
XX	PN	WO200057182-A2.	PR	27-SEP-2000;	2000US-0231584
XX	XX		PR	27-SEP-2000;	2000US-0231596
XX	XX		PR	29-SEP-2000;	2000US-0231607
XX	PD		PR	29-SEP-2000;	2000US-0231668
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XX	XX		PR	17-NOV-2000;	2000US-0249279
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XX	XX		PR	08-DEC-2000;	2000US-0251856
XX	XX		PR	08-DEC-2000;	2000US-0251868
XX	XX		PR	08-DEC-2000;	2000US-0251893

01-SEP-2000; 2000DF-1043926;
(EPIC-) EPIGENOMICS AG;
Olek A, Piepenbrock C, Berlin K;
WPI; 2002-147896/19;
Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction -
Claim 1: SEQ ID No 333; 24pp: English.
The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a substitution of sulphhydryl, hydrogen sulphate or isomers thereof, a substitution of methyl groups, a substitution of methyl groups for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The claim contains DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebrospinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, and a method for the diagnosis and/or therapy of genetic and epigenetic sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. AKI3159, AKI31545 represent chemically pretreated genomic DNA and AKI3159, AKI31545 represent chemically associated with signal transduction, or their complementary sequences.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
Sequence 6102 BP: 1572 A; 95 C; 1468 G; 2877 T; 0 other;
Query Match
Query Length 6102, Score 45.9; DB 4; Length 6012;
Query Start 1, Similarity 63.94; Percent 0.0437; Indels 1; Gaps 1;
Matches 85; Conservative 0; Mismatches 47;
588 GTTTCGACGATATTTTCTAACTATTAAATATTTACATGCTGCAATTG 647
1330 CTCATTAATAAATATTTCTAACTATTAAATATTTTACTATATTAATACAA 1772
648 CATATATGTAAGTGCACAAATCTGCTCACTGGCTCAACGATTTTCAATATTC 707
1271 CATATATTAATACGAACTCTTAATACATCAATTAATATTTTACAAATATGAC 1312
708 ACCGATCATCA 720
1211 ACCGATCAATCA 1199
RESULT 10
AAI20957
ID AAI20997 standard; cDNA; 809 BP.
XX AAI20957;
XX AAI20997;
XX 07-DEC-2001 (first entry)
XX Human breast cancer expressed polynucleotide 13154.
XX Human: breast cancer; cell marker; cytostatic; ss.
XX Homo sapiens.
XX W0200151628-A2.
XX 19-JULY-2001.
XX 10-JAN-2001; 2001WO-US00798.
XX

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XX 14-JAN-2000: 2000US-0176077-
PR 14-MAR-2000: 2000US-0189167-
PR 24-MAR-2000: 2000US-0192099-
PR 24-MAR-2000: 2000US-0192099-
PR 15-MAY-2000: 2000US-0205230-
PR 09-JUN-2000: 2000US-0211315-
PR 25-JUL-2000: 2000US-0220534-
PA (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J. Xu Y. Wang Y. Steinmann K.
XX
XX HPI: 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -
XX
XX Claim 1, Page 3389; 3659pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAU07543 AA226789) and methods of assessing whether a patient is
CC potentially at risk of breast cancer by determining the correlation between the
CC expression of breast cancer genes and the expression of the polynucleotides.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX Sequence 809 BP: 193 A; 213 C; 188 G; 212 T; 3 other;
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XX Query Match 6.1%; Score 45.6; DB 32; Length 809;
XX Best Local Similarity 63.9%; Pred. No. 0.23;
XX Matches 69; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
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DB
XX 388 ATGTAAATACCAAAAGTGCATACATACATGCTGACATGCTCATGAGTTTTCACGCG 447
XX
XX 703 TTTCACCATGCTATACGACGAGTCTACATGATAGTATGATGCT 750
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XX 448 TTATACACCTGCTAGTACGACCCGCGCCACAAAGAAAGATGTTCCCT 495
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XX RESULT 11
XX AAS39742
XX D AAS39742 standard; DNA; 3619 bp
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XX AC AAS39742;
XX
XX 17-DEC-2001 (first entry)
XX
XX Genomic sequence #161 encoding human colon associated polypeptide.
XX
XX Human; colon cancer; congenital abnormality; infection; colitis;
XX intestinal; inflammatory disorder; neoplasia; benign neoplasia;
XX sigmoid disease; antibacterial; antiviral; antiinflammatory;
XX cytostatic; ds.
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XX Homo sapiens.
XX
XX W0200153302-A2.
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XX 02-AUG-2001.
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XX 17-JAN-2001; 2001MO-US01240.
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XX 31-JAN-2000; 2000US-0178065-
XX 04-FEB-2000; 2000US-0180658-
XX 24-FEB-2000; 2000US-0184654-
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XX 02-MAR-2000; 2000US-0186630-
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Search completed: April 11, 2003, 20:09:56
Job time : 257.63 secs

[illegible]

REFERENCE	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo: 1 (bases 1 to 375)
AUTHORS	Adams M.D., Runcie, S.D., Field C.E., Bass, S., Linher, R., Golden, A.M., K. J. Granger, B., Sun, S., White, C., Shizuya, H., Simon, J., and Venter, J. A. 1997
TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Building a Human Genome Map (1997)
COMMENT	Other-GSSs: C1F-HSP-205416.TR Contact: Mark Adams Department of Genetic Sciences The Institute for Genomic Research 7912 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Email: adams@tigr.org Email: markadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.resgen.org/cdb/humans/bac_end_search/bac_end_search.html Seq. primer: M13-21 Class: BAC ends
FEATURES	Location/Qualifiers 117 a 73 c 55 g 130 t +organism="Homo sapiens" +db_xref="db:0087059121" +db_xref="taxon:9606" +clone_id="C1F-HSP" +sex="Male" +note="BAC" "Spasm" +note="BAC": pBioBAC11; Site_1: HindIII; Site_2: HindIII
BASE COUNT	117 a 73 c 55 g 130 t
ORIGIN	6.3k: Score: 47.4; DB 17: Length: 375; Best Local Similarity 62.0k: Pred. No. 0.066; Indels 0: Gaps 0: Matches 75: Conservative 0: Mutations 46:
QY	620 TTTAAATATTAACATGCTACATCTTCATATGATGATGGATGCAATCTGCCTACAT 679
DB	219 TTTATCTCTGTTTGATGATTAATATGATCAATCAATCAATCTATCTATTTAGCCCT 278
QY	680 GCGCTACATGATTTTATCATATTCACCACTGATCATCCGCCAGATCTGATGATG 739
DB	276 ATGTCATGATGCTGCATCATGATGATGCACCGTGCACCCATCTAGTTTGGACAC 338
QY	640 A 740
DB	339 A 339
RESULT 15	BH497623
LOCUS	BH497623/5
DEFINITION	BGGQ227R B000 Brassica oleracea genomic clone BGGQ27, DNA
ACCESSION	BH497623
VERSION	BH497623.1 G117705727
KEYWORDS	BRASSICA OLERACEA
SOURCE	Brassica oleracea
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Equisetopsida; Magnoliopsida; Eudicotyledons; core eudicotyledons; Rosids; Malvales; Brassicales; Brassicaceae; Brassica
REFERENCE	1 (bases 1 to 655)
AUTHORS	Town, C.B., Van Aken, S., Utterback, T., and Fraser, C.M.
JOURNAL	Genomic map and sequencing of Brassica oleracea
COMMENT	Unpublished (2001) Other-GSSs: BGGQ27TF Contact: Chris Town 9712 Medical Center Drive, Rockville, MD 20850, USA

GenCore version 5.1.1.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 15:37:18 Search time 20:7101 seconds
11106:080 Million cell updates/sec

Title: us-09-914-152-3_COPY_1_750

Sequence: 1 cgccttcgcaggtacc.....ctagatagaatgattcgt 750

Scoring table: IDENTITY: 100% Gap: 10.0% Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum db seq length: 0

Maximum db seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 43 summaries

Database : Issued Patents: NA.*
1: /cgn2.6/pctdata/1/ina/5A-COMB.seq.*
2: /cgn2.6/pctdata/1/ina/5A-COMB.seq.*
3: /cgn2.6/pctdata/1/ina/5A-COMB.seq.*
4: /cgn2.6/pctdata/1/ina/6E-COMB.seq.*
5: /cgn2.6/pctdata/1/ina/PCRTUS-COMB.seq.*
6: /cgn2.6/pctdata/1/ina/backfillen.seq.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	45.2	5.7	50060	4	US-09-146-083-5	Sequence 6, Appl
2	37.6	5.0	11299	4	US-09-238-136-11	Sequence 14, Appl
3	37.6	5.0	36651	4	US-09-738-984A-13	Sequence 3, Appl
4	37.4	5.0	9171	1	US-09-008-825-5	Sequence 5, Appl
5	37.4	5.0	9171	2	US-08-530-186-5	Sequence 5, Appl
6	37.4	5.0	9171	2	US-08-530-186-5	Sequence 5, Appl
7	37.4	5.0	9171	2	US-08-459-680-5	Sequence 5, Appl
8	37.4	5.0	9171	2	US-08-517-607-5	Sequence 5, Appl
9	37.4	5.0	9171	2	US-08-719-611-5	Sequence 5, Appl
10	37.4	5.0	9171	2	US-08-038-682-6	Sequence 5, Appl
11	37.4	5.0	9171	2	US-08-459-680-6	Sequence 5, Appl
12	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
13	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
14	37.4	5.0	9171	2	US-08-459-680-6	Sequence 5, Appl
15	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
16	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
17	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
18	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
19	37.2	5.0	98844	4	US-09-791-211-10	Sequence 10, Appl
20	36.2	4.8	50000	4	US-09-146-083-4	Sequence 4, Appl
21	35.8	4.7	16250	4	US-09-345-882-14	Sequence 1, Appl
22	35.8	4.7	16250	4	US-09-345-882-14	Sequence 1, Appl
23	35.4	4.7	6623	2	US-08-687-080-68	Sequence 56, Appl
24	35.2	4.7	2368	4	US-08-714-918-2	Sequence 2, Appl
25	35.2	4.7	2368	4	US-08-714-918-2	Sequence 2, Appl
26	35.2	4.7	2368	4	US-09-265-315-2	Sequence 2, Appl
27	35.2	4.7	2368	4	US-09-265-417-2	Sequence 2, Appl

28	35.2	4.7	5596	3	US-08-751-956-21	Sequence 21, Appl
29	35.2	4.7	5596	3	US-08-751-956-21	Sequence 21, Appl
30	34.8	4.6	722	4	US-08-998-416-780	Sequence 780, Appl
31	34.8	4.6	722	4	US-08-998-416-780	Sequence 780, Appl
32	34.8	4.6	722	4	US-08-998-416-780	Sequence 780, Appl
33	34.4	4.5	603	4	US-09-131-001C-1226	Sequence 1226, Appl
34	34.4	4.5	603	4	US-09-131-001C-1226	Sequence 1226, Appl
35	34	4.5	4287	1	US-08-038-682-7	Sequence 7, Appl
36	34	4.5	4287	1	US-08-038-682-7	Sequence 7, Appl
37	34	4.5	4287	1	US-08-038-682-7	Sequence 7, Appl
38	34	4.5	4287	1	US-08-038-682-7	Sequence 7, Appl
39	34	4.5	4287	1	US-08-038-682-7	Sequence 7, Appl
40	33.4	4.5	4287	1	US-08-728-470-7	Sequence 7, Appl
41	33.4	4.5	4287	1	US-08-728-470-7	Sequence 7, Appl
42	33.6	4.5	1215	4	US-09-321-851-8	Sequence 8, Appl
43	33.2	4.4	2547	3	US-08-265-220-7	Sequence 7, Appl
44	33.2	4.4	2547	3	US-08-471-733-7	Sequence 7, Appl
45	33.2	4.4	2547	3	US-08-471-733-7	Sequence 7, Appl
46	33.2	4.4	2547	3	US-08-756-494-7	Sequence 7, Appl

ALIGNMENTS

Result No.	Query	Score	Match	Length	DB ID	Description
1	45.2	5.7	50060	4	US-09-146-083-5	Sequence 6, Appl
2	37.6	5.0	11299	4	US-09-238-136-11	Sequence 14, Appl
3	37.6	5.0	36651	4	US-09-738-984A-13	Sequence 3, Appl
4	37.4	5.0	9171	1	US-09-008-825-5	Sequence 5, Appl
5	37.4	5.0	9171	2	US-08-530-186-5	Sequence 5, Appl
6	37.4	5.0	9171	2	US-08-530-186-5	Sequence 5, Appl
7	37.4	5.0	9171	2	US-08-459-680-5	Sequence 5, Appl
8	37.4	5.0	9171	2	US-08-517-607-5	Sequence 5, Appl
9	37.4	5.0	9171	2	US-08-719-611-5	Sequence 5, Appl
10	37.4	5.0	9171	2	US-08-038-682-6	Sequence 5, Appl
11	37.4	5.0	9171	2	US-08-459-680-6	Sequence 5, Appl
12	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
13	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
14	37.4	5.0	9171	2	US-08-459-680-6	Sequence 5, Appl
15	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
16	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
17	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
18	37.4	5.0	9171	2	US-08-530-186-6	Sequence 5, Appl
19	37.2	5.0	98844	4	US-09-791-211-10	Sequence 10, Appl
20	36.2	4.8	50000	4	US-09-146-083-4	Sequence 4, Appl
21	35.8	4.7	16250	4	US-09-345-882-14	Sequence 1, Appl
22	35.8	4.7	16250	4	US-09-345-882-14	Sequence 1, Appl
23	35.4	4.7	6623	2	US-08-687-080-68	Sequence 56, Appl
24	35.2	4.7	2368	4	US-08-714-918-2	Sequence 2, Appl
25	35.2	4.7	2368	4	US-08-714-918-2	Sequence 2, Appl
26	35.2	4.7	2368	4	US-09-265-315-2	Sequence 2, Appl
27	35.2	4.7	2368	4	US-09-265-417-2	Sequence 2, Appl

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> CURRENT FILLING DATE: 1998-05-02
> EARLIER FILLING DATE: 1997-05-02
> NUMBER OF SEQ ID NOS: 7
> SOURCE: Genbank Ver. 2.0
> SEQ ID NO 3: Genbank Ver. 2.0
> LENGTH: 50000
> ORGANISM: Homo sapiens
> TITLE: HLA-DQA1*01:01
> ORGANISM: Homo sapiens
> US-09-146-053-3

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Best Local Similarity 5.7%; Score 42.6; DB 4; Length 50000;
Matches 72; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

> 615 ACTTATTAAGAAATATATACCTGCTACATTCGCTATGAGTGAAGTGCCTGCTCC 674
> 26257 AATTTTAAACAGTGTATGAGATCAATTTTACATATATATGAGTGTTCATCAAG 26316
> 675 TACATGCTCGATGATTTTACATATATTCACCCATGTCATCCAGCATGATCAAGTAC 734
> 26317 TGTCAATATTTGACAGGTTTCATATATATGTAGAGCTTCCTGTAACCATCAACATCAAG 26376
> 735 A 735
> 26377 A 26377

RESULT 3
US-09-238-356-14/c Location US/09238356
Patent No. 6312685
GENERAL INFORMATION:
APPLICANT: Kingman, et al.
FILE REFERENCE: 74523-2006
CURRENT APPLICATION NUMBER: US/09/238,356
CURRENT FILLING DATE: 1999-04-27
PRIORITY DATE: 1998-04-27
PRIORITY NUMBER: PCT/US/03876
PRIORITY FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 64
US-09-238-356-14 Patent version 3.0
SEQ ID NO 3:
LENGTH: 11299
TYPE: DNA
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: (1)..(11299)
LOCUS: (1)..(11299)
DATE OF DEPOSITION: 1998-04-27
DATABASE ACCESSION NUMBER: AX001394
DATABASE ENTRY DATE: 2000-08-24
RELEVANT RESIDUES: (1)..(11299)
US-09-238-356-14

Query Match
Best Local Similarity 5.0%; Score 37.6; DB 4; Length 11299;
Matches 100; Conservative 0; Mismatches 169; Indels 1; Gaps 1;

> 617 ACCAATGATGTGTAAAGACCTGCAAGACTTCAGCTGACGAAAAGCAACTCC 476
> 6893 GCACATATAGACATGACCTGCAAGACCTTACAGCTGACGCTACATGCTGCT 6894
> 477 AGCACTTTATCTCGAATCTGTGTTGTGAGCACTGCGCATGGAATGCTCCGAGA 536
> 6833 ATGCACTATACCAACAACTTCTGATGCTATGCTATGCTGATGCTGATGAGAGA 6774
> 537 ATAGTGGATTTGGTCAATTAATTTGGCAATTTGCAAGATTCACAGACATGTGCTTCAG 596
> 6773 ATAGTGAAGAGATGATGCAAGACTTACTTACTTACTTACTTACTTACTTCTGTTG 6714
> 597 AGATTATTTTAACTATTTTAAATATTTAAATATTTAAAGAGTGA-CAATTGCTGATAG 655
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DB 6713 TTATTATACAGAGATTAATTTGGTTAAAGCTTCTATTAATGTAGAGTATTATCA 5654
QY 656 GAAGTGTGCACAACTTCGCTACATGCTGCTCAATGATTTTACATATATTTCCACCAT 715
> 6565 TATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 6594
QY 716 ATATCCACGACGAGATCTAGA 735
DB 6593 AGCAACCCCAACATCTGATA 6574

RESULT 4
US-09-738-894A-3/c
Sequence 3, Application US/09738894A
Patent No. 6311423
APPLICANT: GIBLER, Karl et al.
FILE REFERENCE: 74523-2006
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
OF SUCH MOLECULES
FILE REFERENCE: CLO00636
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
US-09-738-894A-3 Patent version 4.0
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 36651
TYPE: DNA
FEATURE:
NAME/KEY: misc_feature
LOCUS: (1)..(36651)
LOCUS: (1)..(36651)
OTHER INFORMATION: n - A.T.C or G
US-09-738-894A-3

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Matches 70; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

> 627 TATTTATGCTGACAAATTTTCATATATGCTGCTGCAATCTTCGCTACGCTCA 486
DB 24765 ATTTTATGATCAATTAATTAATCAATCAATCAATCAATCAATCAATCAATCAAT 24766
QY 657 TGAGTTTTCATATATTTCCACCATGATATACCAAGAGCTAGATAGATGAT 745
DB 24705 TGAATTTTAAATTAATTAATGAGCTTCAATTAATCAACCAACCAACCAACCAAT 24646
QY 747 TCTT 750
DB 24645 TCTT 24642

RESULT 5
US-08-038-482-5/c Application US/0803862
Patent No. 5545857
GENERAL INFORMATION:
APPLICANT: STEVEN J. JOSEPH W
FILE REFERENCE: 74523-2006
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
OF NON-TYPEABLE HAMPHILUS
US-08-038-482-5 Patent version 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shomaker and Matzare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
CITY: Arlington, VA 22202-4302
STATE: Virginia
COUNTRY: U.S.A.
COMPUTER FILE NAME: US-08-038-482-5
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentID Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/038,682
: FILING DATE: 16-MAR-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: BERKSTRESSER, JERRY W
: TELEPHONE: (703) 415-0810
: TELEFAX: (703) 415-0810
: REFERENCE/DOCKET NUMBER: 1038-293
: TELECOMMUNICATION INFORMATION:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9171 base pairs
: TYPE: H: doublet, single
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-018-682-5

Query Match          5.0%: Score 37.4; DB 1: Length 9171;
Best Local Similarity 48.0%: Pred. No. 0.38;
Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTTGAGACACCGCCACCAATGCTCTCCAGAAATAGTGATTTGGTCAAA 557
DB 5191 GTTTCAGTCCACCAACAGATGAGCTTTTACTTAAAGCTTTTAACTACAT 5132
QY 558 TAAATTTGGGCAATCTACAGACATGCTGTTTTTACAGATTTATTTTAATAACT 617
DB 5131 GATGAAACACCGCAGCAACTGATATGATATGCTGATGTTTAACTGTTTATA 5072
QY 618 TATTAAATTAATACATGCTGATATGCAATATGAGTGCGCAATCTTGGCTAC 677
DB 5071 TTTTTCATATATACCTGTTAAATATGCTATGATGTTCTGCTGTTTATTAAG 5012
QY 678 ATGGCTCAATGAGTTTACATATATATTCACCACTGATATCA 720
DB 5011 ATGGGTAAAGCCGCTAGCTTAACTTAAACCAACAGTAATAA 4969

RESULT 6
US-08-302-832-5/C
: Sequence 5: Application US/08102832
: GENERAL INFORMATION:
: APPLICANT: Barenkamp, Stephen J
: TITLE OF INVENTION: High Molecular Weight Surface Proteins
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Shoemaker and Davtare, Ltd
: STREET: 100 Jefferson Davis Hwy., 1203 Crystal Plaza
: CITY: Arlington
: STATE: Virginia
: ZIP: 22202-0286
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentID Release #1.0, Version #1.30
: APPLICATION NUMBER: US/08/102,832
: FILING DATE: 16-MAR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: US PCT/US93/02166
: FILING DATE: 16-MAR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Berkstresser, Jerry W
: TELEPHONE: (703) 415-0810
: REFERENCE/DOCKET NUMBER: 1038-404
: TELECOMMUNICATION INFORMATION:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9171 base pairs
: TYPE: H: doublet, single
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-302-832-5

Query Match          5.0%: Score 37.4; DB 1: Length 9171;
Best Local Similarity 48.0%: Pred. No. 0.38;
Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTTGAGACACCGCCACCAATGCTCTCCAGAAATAGTGATTTGGTCAAA 557
DB 5191 GTTTCAGTCCACCAACAGATGAGCTTTTACTTAAAGCTTTTAACTACAT 5132
QY 558 TAAATTTGGGCAATCTACAGACATGCTGTTTTTACAGATTTATTTTAATAACT 617
DB 5131 GATGAAACACCGCAGCAACTGATATGATATGCTGATGTTTAACTGTTTATA 5072
QY 618 TATTAAATTAATACATGCTGATATGCAATATGAGTGCGCAATCTTGGCTAC 677
DB 5071 TTTTTCATATATACCTGTTAAATATGCTATGATGTTCTGCTGTTTATTAAG 5012
QY 678 ATGGCTCAATGAGTTTACATATATATTCACCACTGATATCA 720
DB 5011 ATGGGTAAAGCCGCTAGCTTAACTTAAACCAACAGTAATAA 4969

RESULT 7
US-08-510-198-5/C
: Sequence 5: Application US/08530198
: GENERAL INFORMATION:
: APPLICANT: Barenkamp, Stephen J
: TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Shoemaker and Davtare, Ltd
: STREET: 100 Jefferson Davis Hwy., 1203 Crystal Plaza
: CITY: Arlington
: STATE: Virginia
: ZIP: 22202-0286
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentID Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/510,198
: FILING DATE: 13-DEC-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: BARENKAMP, STEPHEN J
: REFERENCE/DOCKET NUMBER: 22,651
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 415-0810
: TELEFAX: (703) 415-0813

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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-530-156-5

Query Match
Best Local Similarity 48.0%; Pred. No. 0.38; Length 9171;
Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTTGAGACAGTGGCCCAAGATGCTCCGAGAAATGTCGATTCGTGTGCAAA 557
DB 5191 GTTTTGAGACAGTGGCCCAAGATGCTCCGAGAAATGTCGATTCGTGTGCAAA 5132
QY 558 TAAATTTGGGCATCTTCAGACAGCATGTCGTTTTCAGAGATTTATTTTAATTAAC 617
DB 531 GATGAGAAAGCCGACAGCAATGATTCGATCAAGATTTATCTGCTTTTATA 5072
QY 618 TATTTAAATATTAATGATGCTGATCAATGATTCGATCAAGATGTCGATTCGTGTGCA 677
DB 5071 TTTTTCATATTAATGATGCTGATCAATGATTCGATCAAGATGTCGATTCGTGTGCA 6012
QY 678 ATGCTCATGATGAGTTTATCAATATTTCCACCATGATCA 720
DB 5011 ATGGGTAAAGCCGCTACTGAACTTAAACCCAGCAAGTAATA 4969

RESULT 8

US-08-469-880-5/C

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Sequence 5, Application US/08469880

Sequence 5, Application US/08469880

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Sequence 5, Application US/08469880

SEQUENCE CHARACTERISTICS:
LENGTH: 9171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-880-5

Query Match
Best Local Similarity 48.0%; Pred. No. 0.38; Length 9171;
Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTTGAGACAGTGGCCCAAGATGCTCCGAGAAATGTCGATTCGTGTGCAAA 557
DB 5191 GTTTTGAGACAGTGGCCCAAGATGCTCCGAGAAATGTCGATTCGTGTGCAAA 5132
QY 558 TAAATTTGGGCATCTTCAGACAGCATGTCGTTTTCAGAGATTTATTTTAATTAAC 617
DB 531 GATGAGAAAGCCGACAGCAATGATTCGATCAAGATTTATCTGCTTTTATA 5072
QY 618 TATTTAAATATTAATGATGCTGATCAATGATTCGATCAAGATGTCGATTCGTGTGCA 677
DB 5071 TTTTTCATATTAATGATGCTGATCAATGATTCGATCAAGATGTCGATTCGTGTGCA 6012
QY 678 ATGCTCATGATGAGTTTATCAATATTTCCACCATGATCA 720
DB 5011 ATGGGTAAAGCCGCTACTGAACTTAAACCCAGCAAGTAATA 4969

RESULT 9

US-08-470-5/C

Sequence 5, Application US/08728470

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Sequence 5, Application US/08728470

Sequence 5, Application US/08728470

Sequence 5, Application US/08728470

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1  LENGTH: 9171 base pairs
2  MOLECULE TYPE: DNA (genomic)
3  STRANDEDNESS: single
4  TOPOLOGY: linear
5  US-08-789-470-5
6
7  Query Match
8  Best Local Similarity 5.0%: Score 37.4; DB 2: Length 9171;
9  Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0.
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11  QY 498 GTTTTGAGACATGCGCCATGAATGCTCTCCGAGAAATAGCGAATTTGGTCAAA 557
12  DB 5131 GTTTTGAGACATGCGCCATGAATGCTCTCCGAGAAATAGCGAATTTGGTCAAA 5132
13  QY 558 TAAATTTGGCAATTCACAGACATGCTCTTTTCAGAGATTTATTTTAAATAACT 617
14  DB 5131 GTTGAAGAGCCGCGACACATGATATGATATTCCTCTCTGCTACAT 5132
15  QY 618 TATTAAATAATTAACATGATGCTCTTTTCAGAGATTTATTTTAAATAACT 677
16  DB 5131 TATTAAATAATTAACATGATGCTCTTTTCAGAGATTTATTTTAAATAACT 677
17  QY 678 ATGGCTCAATGATTTTACATATATTCACCATGATCA 720
18  DB 5011 ATGGCTCAATGATTTTACATATATTCACCATGATCA 720
19
20  RESULT 11
21  US-08-719-641-5/C
22  ; Sequence 5, Application US/08719641
23  ; Patent No. 621841
24  ; GENERAL INFORMATION:
25  ; APPLICANT: Barenkamp, Stephen J
26  ; TITLE OF INVENTION: High Molecular Weight Surface Proteins
27  ; NUMBER OF SEQUENCES: 11 No. 597336-Typeable Haemophilus
28  ; CORRESPONDENCE ADDRESS:
29  ; ADDRESSEE: Shoemaker and Mattare, Ltd
30  ; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
31  ; CITY: Arlington
32  ; STATE: Virginia
33  ; COUNTRY: U.S.A.
34  ; POSTAL CODE: 22202-0286
35  ; COMPUTER READABLE FORM:
36  ; MEDIUM TYPE: Floppy disk
37  ; SOFTWARE: IBM PC compatible
38  ; OPERATING SYSTEM: PC-DOS/MS-DOS
39  ; CURRENT APPLICATION DATA:
40  ; FILING DATE: 01-APR-1996
41  ; CLASSIFICATION: 424
42  ; PRIOR APPLICATION DATA:
43  ; FILING DATE: 05-OCT-1994
44  ; APPLICATION NUMBER: US 08/092,832
45  ; PRIORITY DATE: 05-OCT-1994
46  ; APPLICATION NUMBER: US PCT/US93/02166
47  ; FILING DATE: 16-MAR-1993
48  ; ATTORNEY/AGENT INFORMATION:
49  ; NAME: Berkstrasser, Jerry N
50  ; ADDRESS: 10000 N. 22nd St., Suite 200, Phoenix, AZ 85028-1018-157
51  ; TELEPHONE: (703) 415-0810
52  ; TELEFAX: (703) 415-0813
53  ; INFORMATION FOR SEQ ID NO: 5:
54  ; SEQUENCE CHARACTERISTICS:
55  ; LENGTH: 9171 base pairs
56  ; STRANDEDNESS: single
57  ; TOPOLOGY: linear
58  ; MOLECULE TYPE: DNA (genomic)
59
60  ; Sequence 5, Application US/08719641
61  ; Patent No. 621841
62  ; GENERAL INFORMATION:
63  ; APPLICANT: Barenkamp, Stephen J
64  ; TITLE OF INVENTION: High Molecular Weight Surface Proteins
65  ; NUMBER OF SEQUENCES: 11 No. 621841-Typeable Haemophilus
66  ; CORRESPONDENCE ADDRESS:
67  ; ADDRESSEE: Shoemaker and Mattare, Ltd
68  ; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
69  ; CITY: Arlington
70  ; STATE: Virginia
71  ; COUNTRY: U.S.A.
72  ; POSTAL CODE: 22202-0286
73  ; COMPUTER READABLE FORM:
74  ; MEDIUM TYPE: Floppy disk
75  ; SOFTWARE: IBM PC compatible
76  ; OPERATING SYSTEM: PC-DOS/MS-DOS
77  ; CURRENT APPLICATION DATA:
78  ; FILING DATE: 01-APR-1996
79  ; CLASSIFICATION: 530
80  ; PRIOR APPLICATION DATA:
81  ; FILING DATE: 05-OCT-1994
82  ; APPLICATION NUMBER: US 08/302,832
83  ; PRIORITY DATE: 05-OCT-1994
84  ; APPLICATION NUMBER: US PCT/US93/02166
85  ; FILING DATE: 16-MAR-1993
86  ; ATTORNEY/AGENT INFORMATION:
87  ; NAME: Berkstrasser, Jerry N
88  ; ADDRESS: 10000 N. 22nd St., Suite 200, Phoenix, AZ 85028-1018-157
89  ; TELEPHONE: (703) 415-0810
90  ; TELEFAX: (703) 415-0813
91  ; INFORMATION FOR SEQ ID NO: 5:
92  ; SEQUENCE CHARACTERISTICS:
93  ; LENGTH: 9171 base pairs
94  ; STRANDEDNESS: single
95  ; TOPOLOGY: linear
96  ; MOLECULE TYPE: DNA (genomic)

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US-08-719-441-5

Query Match 5.04: Score 37.4; Db 4: Length 9171;

Best Local Similarity 48.04; Pred. No. 0.38; Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTGGAGACGGCCCAATGATGCTCCCAAGAAATGTCGAAATGTCGCAAA 557

Db 5191 GTTTCAGTCGACGATGACGAGGCTTTTACTAAAGCGCTCTCTCGCATACAT 5132

QY 558 TAAATTTGGCAATCTACAGACATGCTCTTTTCAGAAATTTTATTAATTAAC 617

Db 5131 GATGAGAGACCGCCAGCAATGATGCTCTTTTATGCTCTTTTATA 5072

QY 618 TATTATAAATATTAACATGCAATTTGCAATGATGCAATGTCGAAATCTTCGTAC 677

Db 5071 TTTTTCATATAATAGCTTAAATAAGCTTATGATGTCGGAATTTTITACAG 4012

QY 678 ATGTCATGATGCTTTTACATATTTATTCACATATTTACACCATATATCA 720

Db 5011 ATGCGTAAAGCGTACTGACTTATACCCACACGTAATA 4969

RESULT 12

US-08-018-682-6/C

Sequence 6, Application US/0803682

Patent No. 5603938

GENERAL INFORMATION:

APPLICANT: BARENKAMP, STEPHEN J

INVENTOR: ST. GENE III, JOSEPH W

TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS

TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS: and Mattare, Ltd

STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202-0286

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/038,682

FILING DATE: 16-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BERNSTRESSER, JERRY W

REGISTRATION NUMBER: 22,651

TELEPHONE: (703) 415-0813

INVESTOR: (703) 415-0813

SEQUENCE CHARACTERISTICS: 61

LENGTH: 9323 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-038-682-6

Query Match 5.04: Score 37.4; Db 1: Length 9323;

Best Local Similarity 48.04; Pred. No. 0.38;

Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTGGAGACGGCCCAATGATGCTCCCAAGAAATGTCGAAATGTCGCAAA 557

Db 5002 GTTTCAGTCGACGATGACGAGGCTTTTACTAAAGCGCTCTCTCGCATACAT 5443

QY 558 TAAATTTGGCAATCTACAGACATGCTCTTTTCAGAAATTTTATTAATTAAC 617

Db 5442 GATGAGAGACCGCCAGCAATGATGCTCTTTTATGCTCTTTTATA 5383

US-08-038-682-6

Query Match 5.04: Score 37.4; Db 1: Length 9323;

Best Local Similarity 48.04; Pred. No. 0.38;

Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTGGAGACGGCCCAATGATGCTCCCAAGAAATGTCGAAATGTCGCAAA 557

Db 5002 GTTTCAGTCGACGATGACGAGGCTTTTACTAAAGCGCTCTCTCGCATACAT 5443

QY 558 TAAATTTGGCAATCTACAGACATGCTCTTTTCAGAAATTTTATTAATTAAC 617

Db 5442 GATGAGAGACCGCCAGCAATGATGCTCTTTTATGCTCTTTTATA 5383

US-08-038-682-6

Query Match 5.04: Score 37.4; Db 1: Length 9323;

Best Local Similarity 48.04; Pred. No. 0.38;

Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTGGAGACGGCCCAATGATGCTCCCAAGAAATGTCGAAATGTCGCAAA 557

Db 5002 GTTTCAGTCGACGATGACGAGGCTTTTACTAAAGCGCTCTCTCGCATACAT 5443

QY 558 TAAATTTGGCAATCTACAGACATGCTCTTTTCAGAAATTTTATTAATTAAC 617

Db 5442 GATGAGAGACCGCCAGCAATGATGCTCTTTTATGCTCTTTTATA 5383

US-08-038-682-6

QY 558 TAAATTTGGCAATCTACAGACATGCTCTTTTCAGAAATTTTATTAATTAAC 617

Db 5442 GATGAGAGACCGCCAGCAATGATGCTCTTTTATGCTCTTTTATA 5383

QY 618 TATTATAAATATTAACATGCAATTTGCAATGATGCAATGTCGAAATCTTCGTAC 677

Db 5191 GTTTCAGTCGACGATGACGAGGCTTTTACTAAAGCGCTCTCTCGCATACAT 5132

QY 558 TAAATTTGGCAATCTACAGACATGCTCTTTTCAGAAATTTTATTAATTAAC 617

Db 5131 GATGAGAGACCGCCAGCAATGATGCTCTTTTATGCTCTTTTATA 5072

QY 618 TATTATAAATATTAACATGCAATTTGCAATGATGCAATGTCGAAATCTTCGTAC 677

Db 5071 TTTTTCATATAATAGCTTAAATAAGCTTATGATGTCGGAATTTTITACAG 4012

QY 678 ATGTCATGATGCTTTTACATATTTATTCACATATTTACACCATATATCA 720

Db 5011 ATGCGTAAAGCGTACTGACTTATACCCACACGTAATA 4969

RESULT 13

US-08-038-682-6/C

Sequence 6, Application US/0803682

Patent No. 5603938

GENERAL INFORMATION:

APPLICANT: BARENKAMP, STEPHEN J

INVENTOR: ST. GENE III, JOSEPH W

TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS

TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS: and Mattare, Ltd

STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202-0286

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/302,832

FILING DATE: 16-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BERNSTRESSER, JERRY W

REGISTRATION NUMBER: 22,651

TELEPHONE: (703) 415-0813

INVESTOR: (703) 415-0813

SEQUENCE CHARACTERISTICS: 61

LENGTH: 9323 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-302-832-6

Query Match 5.04: Score 37.4; Db 1: Length 9323;

Best Local Similarity 48.04; Pred. No. 0.38;

Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 498 GTTTGGAGACGGCCCAATGATGCTCCCAAGAAATGTCGAAATGTCGCAAA 557

Db 5002 GTTTCAGTCGACGATGACGAGGCTTTTACTAAAGCGCTCTCTCGCATACAT 5443

QY 558 TAAATTTGGCAATCTACAGACATGCTCTTTTCAGAAATTTTATTAATTAAC 617

Db 5442 GATGAGAGACCGCCAGCAATGATGCTCTTTTATGCTCTTTTATA 5383

QY 618 TATTATAAAATTAACAGTGCACATTCGATGATGAGAGTGTGCAATCTTCGCTAC 677
 Db 5382 TTTTTCATATATTAACCTCTTAAATTAATCTTTATGATCTTCCTGTAATTTTACAG 5323
 QY 678 ATGGCTCAATGCTTTTACATATATATTCACCCACGATCA 720
 Db 5322 ATGGGTAAAGCCCTACTGACTTTTAAACCCACGATCAATTA 5280
 RESULT 14
 US-08-530-198 6/C Location US/08530198
 : Sequence 6, Application US/0846980
 : Patent No. 5859065
 : GENERAL INFORMATION:
 : APPLICANT: BARENKAMP, STEPHEN J.
 : TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
 : TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
 : TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Shoemaker and Maltare, Ltd
 : STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202-0286
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA: US/08/530.198
 : FILING DATE: 06-JUN-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : REFERENCE/DOCKET NUMBER: JWB-1186
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 415-0810
 : INFORMATION FOR SEQ ID NO: 6:
 : TYPE: nucleic acid
 : LENGTH: 9323 base pairs
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : US-08-530-198 6
 Query Match 5.08; Score 37.4; Db 2; Length 9323;
 Best Local Similarity 48.00; Pred No. 0.38;
 Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
 QY 498 GTTTGTGAGACCTGCCTCCATATCTCTCCGCAAAATTCGGATTTGTGTGAA 557
 Db 5502 GTTTCAGTGCACCATCACTGATGAGCTTTTAAAGCTCTCTCTCAAT 5443
 QY 558 TAAATTTGGCCTATTCAGACAGCTGTCTTTTTCAGATATTTATTTAAATCT 617
 Db 5442 GATGAGACGCCGACGACGATATGATATTCGACATGATTTATCTGCTTTTATA 5383
 QY 618 TATTATAAAATTAACAGTGCACATTCGATGATGAGAGTGTGCAATCTTCGCTAC 677
 Db 5382 TTTTTCATATATTAACCTCTTAAATTAATCTTTATGATCTTCCTGTAATTTTACAG 5323
 QY 678 ATGGCTCAATGCTTTTACATATATATTCACCCACGATCA 720
 Db 5322 ATGGGTAAAGCCCTACTGACTTTTAAACCCACGATCAATTA 5280

RESULT 15
 US-08-469-880-6/C
 : Sequence 6, Application US/0846980
 : Patent No. 5859773
 : GENERAL INFORMATION:
 : APPLICANT: BARENKAMP, STEPHEN J.
 : TITLE OF INVENTION: High Molecular Weight Surface Proteins
 : TITLE OF INVENTION: OF NO. 5876733:Typeable Haemophilus
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Shoemaker and Maltare, Ltd
 : STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202-0286
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA: US/08/469.880
 : FILING DATE: 06-JUN-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA: GB 920704.1
 : FILING DATE: 16-MAR-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US PCT/US99/02166
 : FILING DATE: 16-SEP-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Reikreiter, Jerry W
 : REGISTRATION NUMBER: 22,653
 : REFERENCE/DOCKET NUMBER: 1038-516 MIS:vg
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 415-0810
 : INFORMATION FOR SEQ ID NO: 6:
 : TYPE: nucleic acid
 : LENGTH: 9323 base pairs
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : US-08-469-880-6
 Query Match 5.08; Score 37.4; Db 2; Length 9323;
 Best Local Similarity 48.00; Pred No. 0.38;
 Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
 QY 498 GTTTGTGAGACCTGCCTCCATATCTCTCCGCAAAATTCGGATTTGTGTGAA 557
 Db 5502 GTTTCAGTGCACCATCACTGATGAGCTTTTAAAGCTCTCTCTCAAT 5443
 QY 558 TAAATTTGGCCTATTCAGACAGCTGTCTTTTTCAGATATTTATTTAAATCT 617
 Db 5442 GATGAGACGCCGACGACGATATGATATTCGACATGATTTATCTGCTTTTATA 5383
 QY 618 TATTATAAAATTAACAGTGCACATTCGATGATGAGAGTGTGCAATCTTCGCTAC 677
 Db 5382 TTTTTCATATATTAACCTCTTAAATTAATCTTTATGATCTTCCTGTAATTTTACAG 5323
 QY 678 ATGGCTCAATGCTTTTACATATATATTCACCCACGATCA 720
 Db 5322 ATGGGTAAAGCCCTACTGACTTTTAAACCCACGATCAATTA 5280

Search completed: April 11, 2003, 22:43:55
Job time : 137.71 secs




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US-09-764-872-639
; Sequence 639, Application US/09764872
; Publication No. US200301005031A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4135
; PRIOR APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-30
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: SeqMan, Entenlin Ver. 2.0
; SEQ ID NO 619
; LENGTH: 3619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-639
Query Match
; Sequence 619, Score 45.4; DB 9; Length 3619;
; Matches 70; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
US-09-864-761-8570
; Sequence 850, Application US/09864761
; Publication No. US200300543753A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Barzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: A601643X
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 09/832,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: CB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
US-09-864-761-8570
; Sequence 850, Application US/09864761
; Publication No. US200300543753A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Barzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: A601643X
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 09/832,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: CB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
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US-09-764-872-639
; Sequence 639, Application US/09764872
; Publication No. US200301005031A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4135
; PRIOR APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-30
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: SeqMan, Entenlin Ver. 2.0
; SEQ ID NO 870
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-639
Query Match
; Sequence 639, Score 44; DB 10; Length 600;
; Best Local Similarity 58.3%; Pred. No. 0.05;
; Matches 77; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
US-09-864-761-8570
; Sequence 850, Application US/09864761
; Publication No. US200300543753A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Barzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: A601643X
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 09/832,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: CB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
US-09-864-761-8570
; Sequence 850, Application US/09864761
; Publication No. US200300543753A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Barzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: A601643X
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR APPLICATION NUMBER: US 09/832,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: CB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
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Db 227 TGACATCTCAATCAAGA 243
RESULT 7
US-09-901-136-3
: Sequence 97, Application US/09901136
: Patent No. US2003003956A1
: GENERAL INFORMATION:
: APPLICANT: HU, Song et al.
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL001273
: CURRENT APPLICATION NUMBER: US/09/901.136
: NUMBER OF SEQ ID NOS: 4
: NUMBER OF SEQ ID NOS: 4 001-07-10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 319361
: TYPE: DNA
: ORGANISM: Human
: FEATURE: misc-feature
: NAME:
: LOCATION: (1)...(378361)
: OTHER INFORMATION: n = A-T-C or G
US-09-901-136-3
Query Match 5.54; Score 41.8; DB 9; Length 378361;
Best Local Similarity 51.94; Pred. No. 7.3;
Matches 94; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY : 57 ATAAATTGGCAATCTACAGACATGCTGTTCTTCAGAGATTTATTTTATTAAC 616
Db 29238 AGAAATATGCTCCCAATATATCATATCATCTCTCTATGATTAATCTGCTCTCTG 29297
QY 617 TTATTAAATATACATGGTACAAATTCGATATAGTAGTGCAATTCGCTA 676
Db 29298 TTATCT 69357
QY 677 CATGGCTCAATGATTTTACATATATTCACCACTGATATCCACCAAGATCA 736
Db 29358 CTATCTTGATGATTTAGTATTTGATTTATACATACAGTATACACCAAG 29417
QY 737 T 737
Db 29418 T 29418
RESULT 8
US-09-764-960-997
: Sequence 997, Application US/09764860
: Patent No. US20020049453A1
: GENERAL INFORMATION:
: APPLICANT: ROSEN et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC008
: CURRENT APPLICATION NUMBER: US/09/764.860
: CURRENT FILING DATE: 2002-03-07
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 1198
: SOFTWARE: Protein Ver. 2.0
: SEQ ID NO 997
: LENGTH: 290
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-764-960-997
Query Match 5.54; Score 41.4; DB 10; Length 290;
Best Local Similarity 6.84; Pred. No. 2.7;
Matches 63; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 637 GGTCAATTTGCAATAGTGTGCAAAATCTTCGCTACATGCTCAATGAGTTT 595

Db 18 GGTAAAGATTACATACAGTGTGCAAAATCTTCGCTACATGCTCAATGAGTTT 77
QY 697 CATATATTTCACCATGATGTATACACCAAGAGATCTAGA 735
Db 78 GAACTGCTAAAGCTTTTATTTATTCACCAAGCTTTTATTA 116
RESULT 9
US-10-091-504-2274
: Sequence 2274, Application US/10091504
: Patent No. US20030059908A1
: GENERAL INFORMATION:
: APPLICANT: ROSEN et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC007C1
: CURRENT APPLICATION NUMBER: US/10/091.504
: CURRENT FILING DATE: 2002-03-07
: NUMBER OF SEQ ID NOS: 2442
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: Protein Ver. 2.0
: SEQ ID NO 2274
: LENGTH: 1402
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-091-504-2274
Query Match 5.54; Score 41.2; DB 9; Length 1402;
Best Local Similarity 6.44; Pred. No. 4.6;
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 637 GGTCAATTTGCAATAGTGTGCAAAATCTTCGCTACATGCTCAATGAGTTT 596
Db 672 GATATACATGATTTACGTAAGTGCACAGCTGTATTTATAGGCTTCATGATTA 931
QY 697 CATATATTTCACCATGATGTATACACCAAGAGAT 730
Db 932 TATTCATATACCAATCTATCTACCTCCCTCAT 965
RESULT 10
US-10-091-504-2275
: Sequence 2275, Application US/10091504
: Patent No. US20030059908A1
: GENERAL INFORMATION:
: APPLICANT: ROSEN et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC008
: CURRENT APPLICATION NUMBER: US/10/091.504
: CURRENT FILING DATE: 2002-03-07
: NUMBER OF SEQ ID NOS: 2442
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: Protein Ver. 2.0
: SEQ ID NO 2275
: LENGTH: 1402
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-091-504-2275
Query Match 5.54; Score 41.2; DB 9; Length 1402;
Best Local Similarity 6.44; Pred. No. 4.6;
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 637 GGTCAATTTGCAATAGTGTGCAAAATCTTCGCTACATGCTCAATGAGTTT 596
Db 872 GATATACATGATTTACGTAAGTGCACAGCTGTATTTATAGGCTTCATGATTA 931
QY 697 CATATATTTCACCATGATGTATACACCAAGAGAT 730
Db 932 TATTCATATACCAATCTATCTACCTCCCTCAT 965
RESULT 11

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US-10-091-504-2276
: Sequence 2276: Application US/0091504
: Publication No. US2003005908A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC007C1
: CURRENT APPLICATION NUMBER: US/20/091,504
: NUMBER OF SEQ ID NOS: 03-07
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: LENGTH: 1402
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-091-504-2276

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Query Match
Best Local Similarity 5.5%; Score 41.2; DB 9; Length 1402;
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Qy 637 GGTCAATTTGCGATATGAGTATGCGAATCTGCTACGCTCATGATGATTTTA 696
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 872 GATATACTAGTATTCAGTAAGTGCACGCTCTTAATATGAGCTCATGATTA 931
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```

Db 932 TATTCATATACACCGATGTAATCTACCTCCCTCAT 965

RESULT 12
US-09-764-869-2274
: Sequence 2274: Application US/09764869
: Patent No. US2002006152A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, proteins, and Antibodies
: FILE REFERENCE: PC0000000000
: CURRENT APPLICATION NUMBER: US/09/764,869
: CURRENT FILING DATE: 2001-01-17
: Prior Application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 2442
: NUMBER OF SEQ ID NOS: 2442
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2274
: LENGTH: 1402
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-764-869-2274

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Query Match
Best Local Similarity 5.5%; Score 41.2; DB 10; Length 1402;
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Qy 637 GGTCAATTTGCGATATGAGTATGCGAATCTGCTACGCTCATGATGATTTTA 696
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 872 GATATACTAGTATTCAGTAAGTGCACGCTCTTAATATGAGCTCATGATTA 931
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Db 932 TATTCATATACACCGATGTAATCTACCTCCCTCAT 965

RESULT 13
US-09-764-869-2275
: Sequence 2275: Application US/09764869
: Patent No. US2002006152A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC0000000000
: CURRENT APPLICATION NUMBER: US/09/764,869
: CURRENT FILING DATE: 2001-01-17

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: Prior application data removed - refer to PALM or file wrapper
: Publication No. US2002006152A1
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2275
: LENGTH: 1402
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-764-869-2275

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Query Match
Best Local Similarity 5.5%; Score 41.2; DB 10; Length 1402;
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Qy 637 GGTCAATTTGCGATATGAGTATGCGAATCTGCTACGCTCATGATGATTTTA 696
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 872 GATATACTAGTATTCAGTAAGTGCACGCTCTTAATATGAGCTCATGATTA 931
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Db 932 TATTCATATACACCGATGTAATCTACCTCCCTCAT 965

RESULT 14
US-09-764-869-2276
: Sequence 2276: Application US/09764869
: Patent No. US2002006152A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC0000000000
: CURRENT APPLICATION NUMBER: US/09/764,869
: CURRENT FILING DATE: 2001-01-17
: Prior Application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 2444
: NUMBER OF SEQ ID NOS: 2444
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2276
: LENGTH: 1402
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-764-869-2276

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Query Match
Best Local Similarity 5.5%; Score 41.2; DB 10; Length 1402;
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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Qy 637 GGTCAATTTGCGATATGAGTATGCGAATCTGCTACGCTCATGATGATTTTA 696
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Db 872 GATATACTAGTATTCAGTAAGTGCACGCTCTTAATATGAGCTCATGATTA 931
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Db 932 TATTCATATACACCGATGTAATCTACCTCCCTCAT 965

RESULT 15
US-09-954-456-505
: Sequence 2275: Application US/09954456
: Patent No. US2002013057A1
: GENERAL INFORMATION:
: APPLICANT: Young Paul
: TITLE OF INVENTION: Sels
: FILE REFERENCE: 689290-76
: CURRENT APPLICATION NUMBER: US/09/954,456
: CURRENT FILING DATE: 2000-09-18
: Prior Application Number: US/60/233,617
: Prior Filing Date: 2000-09-18
: Prior Application Number: US/60/234,052
: Prior Filing Date: 2000-09-18
: Prior Application Number: US/60/234,923
: Prior Filing Date: 2000-09-25
: Prior Application Number: US/60/235,134
: Prior Filing Date: 2000-09-25

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US-09-914-152-3_copy_1_750_rnpb

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; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
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; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 505
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-505

Query Match      5.4%; Score 40.6; DB 10; Length 3777;
Best Local Similarity 55.2%; Pred. No. 1.2;
Matches 79; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 592 TTCAGAGATTATTTTAAATTAACCTATTAAATAATTAACTGGTACATTCGATA 651
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3303 TTCAGAGCTGATGATCTATCTATCTATTTTAAACACACCTATAGAGGTGATATTATTA 3362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 652 TAGTGAGTGCACAACTTCGTCACATGGCTCAATGAGTTTTCATATATTTCCACCC 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3363 CATATAAATGTTCCACTTAAATATACATTTGATGAGTTTGATTAATGTGATATACC 3422
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 712 ATGTATCACACCGAGATCTAG 734
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3423 AATACACACACCTCCAGTCAG 3445
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Search completed: April 12, 2003, 03:49:48
 Job time : 1005.96 secs

[illegible]

sequence is ambiguous, there is an annotation using the 'unsure' feature key.
 This sequence was generated from part of bacterial clone contigs of the genome of the bacterium *Salmonella enterica* serovar *Paratyphi* phage type *1* (H37Rv) from the Sanger Centre Chromosome I Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chri>
 105652 is from the library APC13 constructed at the Roswell Park Cancer Institute, Buffalo, NY.
 Details see <http://ncic.nci.nih.gov/buffalo/nci/VBC08/GC1902/>

FEATURES

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 2018..2177
 /note="2 copies 80 mer 95% conserved"
 /note="2018-2177"
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 2052..52289
 /note="EST AK01759 clone IMAGE109929"
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 2176..2339
 /note="2 copies 82 mer 85% conserved"
 /note="2021-2339"
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 complement(3220..3167)
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 /note="p185 repeat: matches 247..32 of consensus"
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 complement(3900..3945)
 /note="p185 repeat: matches 1397..1353 of consensus"
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 3987..4286
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 4102..4137
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 repeat_region
 5506..5937
 /note="M22 repeat: matches 8..344 of consensus"
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 /note="match: GSS M5225"
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 /note="L1PA10 repeat: matches 900..662 of consensus"
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 complement(13451..13902)
 /note="ML10 repeat: matches 505..44 of consensus"
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 14327..14444
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 complement(14857..14993)
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 15170..15209
 /note="MERSA repeat: matches 4 mer cont 83% conserved"
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 complement(19889..20167)
 /note="MER31 repeat: matches 302..26 of consensus"
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 24433..24855
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 /note="L1PA15 repeat: matches 904..1 of consensus"
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 complement(25626..26986)
 /note="L1 repeat: matches 5390..3983 of consensus"
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 27000..27155
 /note="L1 repeat: matches 2116..2707 of consensus"
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 /note="AluY repeat: matches 301..34 of consensus"

repeat_region
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 31659..32910
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 32959..33606
 /note="M22 repeat: matches 1..912 of consensus"
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 /note="M18 repeat: matches 247..32 of consensus"
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 36080..36149
 /note="MERSA repeat: matches 4..109 of consensus"
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 /note="15 copies 4 mer gaag 100% conserved"
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 437067..37716
 /note="M18 repeat: matches 146..48 of consensus"
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 /note="match: GSS M5225"
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 /note="AluB repeat: matches 300..1 of consensus"
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 /note="match: multiple ESTs; match: EST 238206 clone c-02h10; paired with EST 241912 matching this clone; match: EST 241912 clone c-02h10; paired with EST 238206 clone c-02h10"
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 38661..38897
 /note="match: STS 005514"
 prim_transcript
 40931..542821
 /note="multiple ESTs; match: M50346 M45495 M31114 A350242 M46781; match: M29818 P04199 H8678 H0505 F07947; match: H05281 F02238 M51569 M4205 M40284; match: H46206 M498020 M51041 M16141 M21157; match: M42769 M5128 H8769 M430243"
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 40991..541471
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 complement(44566..47136)
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 complement(46542..46643)
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 47137..47166
 /note="match: 3' EST AAG85139 clone IMAGE1614277; complement(50606..50641)
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 /note="M18 repeat: matches 301..1 of consensus"
 repeat_region
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 /note="AluY repeat: matches 300..1 of consensus"

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repeat_region complement(57973, 58073)
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repeat_region complement(58080, 58180)
repeat_region /note=AluSc repeat: matches 293, .1 of consensus*
repeat_region complement(62401, 64830)
repeat_region /note=MIR2 repeat: matches 218, .1 of consensus*
repeat_region /note=MIR2 repeat: matches 15, .146 of consensus*
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misc_feature 65839, 66276
/note=match: GSS AQ002124*
repeat_region 67773, 67839 repeat: matches 79, .146 of consensus*
repeat_region 68924, 68987 repeat: matches 64, .146 of consensus*
repeat_region 69306, 70033 repeat: matches 4843, .5389 of consensus*
repeat_region 69693, 70591 repeat: matches 1, .1047 of consensus*
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Query Match 48.3%, Score 362.41, Db 9, Length 100416;
Best local similarity 75.8%; Pred. No. 1,66-65;
Matches 505; Conservative 0; Mismatches 146; Indels 15; Gaps 4;

QY 52 CGACTCATGATTAACATTCAGTGGATGAGAGTGGCTGCTATG-ATGAGAAAGAGG 110
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QY 111 TGGTCTTGATTAAGATGGAATTAATCATGAGATGCTGCTGATGAGATGCTGAGATG 170
Db 63058 TGGTCTTGATTAAGATGGAATTAATCATGAGATGCTGCTGATGAGATGCTGAGATG 170
QY 171 AGAAGATTAATGATGTTACATGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 230
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QY 1998 CAAAGAGTTAGATTAATTCATTAACATTAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 62879
Db 63058 CAAAGAGTTAGATTAATTCATTAACATTAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 62879
QY 231 ATGAGTCTCAATTTAAATTAATGTTCTGCTGGTAAATGATATCAATGAGTGTAGTGTAGTGTAG 290
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QY 351 TGTGACAGAGATTAATCATGAGAGAGAGATCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 410
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QY 468 AAGATGAGAGATCAATGATGAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 527
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Db 63058 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62579
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Db 63058 TAGTGTATTTAGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587
QY 62578 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62519
Db 63058 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62519
QY 368 ATATGATTT--AATATGATGAGAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
Db 63058 ATATGATTT--AATATGATGAGAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
QY 62518 ATATGATTT--AATATGATGAGAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62459
Db 63058 ATATGATTT--AATATGATGAGAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62459
QY 637 TGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
Db 63058 TGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
QY 62519 TGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62399
Db 63058 TGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62399
QY 697 AGAAG 702

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Db 62398 TGCAG 62393
RESULT 9
LOCUS 2000
DEFINITION Homo sapiens chromosome 1 clone RP11-114314, WORKING DRAFT
ACCESSION AC069000
VERSION 158149 bp
KEYWORDS HTGS-PHASE1; HTGS-DRAFT;
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 158149)
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 158149)
TITLE Direct Submission
JOURNAL

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Center Project: Project Information
Center Project: Summary Statistics
Sequencing vector: M13, 100%
Sequencing method: plasmid, 0%
Chemistry: Dye-terminator Big Dye, 0% of reads
Assembly Program: Phrap, version 0.90319
Consensus quality: 15397 bases at least Q40
Consensus quality: 15397 bases at least Q40
Consensus quality: 155094 bases at least Q20
Insert size: 126000; agarose-gel
Quality coverage: 156743.73; 0.000000
Quality coverage: 4.63 in Q20 bases; sum-of-contigs
-----
This sequence was generated by a pipeline that currently
consists of 15 contig-purification steps. The pipeline
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
N's. The lengths of the contigs and the gaps are unknown.
This record will be updated with this information as
soon as it is available and the accession number will
be preserved.
-----
1930: contig of 1930 bp in length
1931: 2030: gap of unknown length
2031: 3803: contig of 1773 bp in length
3804: 3903: gap of unknown length
3904: 5666: gap of unknown length
5667: 5668: gap of unknown length
5669: 10220: contig of 4654 bp in length
10221: 10220: gap of unknown length
10221: 16201: gap of unknown length
16201: 16300: gap of unknown length
16301: 23791: contig of 7491 bp in length
23792: 23810: gap of unknown length
23811: 32710: gap of unknown length
32711: 43891: contig of 11181 bp in length
43892: 43892: gap of unknown length
43893: 53468: gap of unknown length
53469: 53468: gap of unknown length

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PR 22-AUG-2000; 2000US-0236868
PR 23-AUG-2000; 2000US-0237182
PR 23-AUG-2000; 2000US-0237009
PR 30-AUG-2000; 2000US-0238224
PR 01-SEP-2000; 2000US-0239343
PR 01-SEP-2000; 2000US-0239344
PR 05-SEP-2000; 2000US-0239345
PR 05-SEP-2000; 2000US-0239346
PR 05-SEP-2000; 2000US-0239513
PR 06-SEP-2000; 2000US-0230437
PR 06-SEP-2000; 2000US-0239435
PR 08-SEP-2000; 2000US-0239440
PR 08-SEP-2000; 2000US-0231143
PR 08-SEP-2000; 2000US-0231144
PR 08-SEP-2000; 2000US-0231145
PR 08-SEP-2000; 2000US-0231080
PR 09-SEP-2000; 2000US-0232081
PR 09-SEP-2000; 2000US-0232082
PR 14-SEP-2000; 2000US-0232187
PR 14-SEP-2000; 2000US-0232188
PR 14-SEP-2000; 2000US-0232359
PR 14-SEP-2000; 2000US-0232360
PR 14-SEP-2000; 2000US-0232401
PR 14-SEP-2000; 2000US-0233063
PR 14-SEP-2000; 2000US-0233064
PR 14-SEP-2000; 2000US-0233065
PR 21-SEP-2000; 2000US-0234274
PR 21-SEP-2000; 2000US-0234275
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PR 27-SEP-2000; 2000US-0235635
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PR 29-SEP-2000; 2000US-0235637
PR 29-SEP-2000; 2000US-0235638
PR 29-SEP-2000; 2000US-0235639
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PR 02-OCT-2000; 2000US-0237037
PR 02-OCT-2000; 2000US-0237038
PR 13-OCT-2000; 2000US-0239935
PR 13-OCT-2000; 2000US-0239936
PR 20-OCT-2000; 2000US-0240960
PR 20-OCT-2000; 2000US-0241221
PR 20-OCT-2000; 2000US-0241782
PR 20-OCT-2000; 2000US-0241783
PR 20-OCT-2000; 2000US-0241787
PR 20-OCT-2000; 2000US-0241808
PR 20-OCT-2000; 2000US-0241809
PR 01-NOV-2000; 2000US-0241857
PR 08-NOV-2000; 2000US-0246974
PR 08-NOV-2000; 2000US-0246975
PR 08-NOV-2000; 2000US-0246976
PR 08-NOV-2000; 2000US-0246977
PR 08-NOV-2000; 2000US-0246978
PR 08-NOV-2000; 2000US-0246979
PR 08-NOV-2000; 2000US-0246524
PR 08-NOV-2000; 2000US-0246525
PR 08-NOV-2000; 2000US-0246526
PR 08-NOV-2000; 2000US-0246527
PR 08-NOV-2000; 2000US-0246528
PR 08-NOV-2000; 2000US-0246529
PR 08-NOV-2000; 2000US-0246530
PR 08-NOV-2000; 2000US-0246531
PR 17-NOV-2000; 2000US-0249207
PR 17-NOV-2000; 2000US-0249208
PR 17-NOV-2000; 2000US-0249209
PR 17-NOV-2000; 2000US-0249210
PR 17-NOV-2000; 2000US-0249211
PR 17-NOV-2000; 2000US-0249212
PR 17-NOV-2000; 2000US-0249213
PR 17-NOV-2000; 2000US-0249214
PR 17-NOV-2000; 2000US-0249215
PR 17-NOV-2000; 2000US-0249216
PR 17-NOV-2000; 2000US-0249217
PR 17-NOV-2000; 2000US-0249218
PR 17-NOV-2000; 2000US-0249244
PR 17-NOV-2000; 2000US-0249245
PR 17-NOV-2000; 2000US-0249246
PR 17-NOV-2000; 2000US-0249247
PR 17-NOV-2000; 2000US-0249248
PR 17-NOV-2000; 2000US-0249249
PR 01-DEC-2000; 2000US-0250297
PR 01-DEC-2000; 2000US-0250298
PR 01-DEC-2000; 2000US-0250391
PR 05-DEC-2000; 2000US-0251030
PR 05-DEC-2000; 2000US-0251031
PR 05-DEC-2000; 2000US-0251032
PR 06-DEC-2000; 2000US-0251479
PR 06-DEC-2000; 2000US-0251480
PR 06-DEC-2000; 2000US-0251481
PR 08-DEC-2000; 2000US-0251856
PR 08-DEC-2000; 2000US-0251857
PR 08-DEC-2000; 2000US-0251858
PR 08-DEC-2000; 2000US-0251859
PR 15-DEC-2000; 2000US-0251990
PR 15-DEC-2000; 2000US-0251991
PR 05-JAN-2001; 2001US-02519678
XX
XX (HUMAN) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition .
XX
XX Disclosure: SEQ ID NO 7972; 1287Pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX polypeptide having a reproductive system related antigens. These can be used
XX in the prevention, treatment or amelioration of reproductive system
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
XX
XX Sequence 4503 BP; 1360 A; 837 C; 792 G; 1514 T; 0 other;
Query Match 39.9%; Score 300; DB 22; Length 4503;
Query Match Similarity 64%; Re-6-22; Mismatches 180; Indels 19; Gaps 5;
Matches 477; Conservative
QY 52 GCATCTCATGAAACTTGGATGAGAGCTGCTCTAT-GATGACAAGAAGG 110
Db 764 CAATCTCATGAAACTTGGATGAGAGCTGCTCTATGATGAGAGAGAGG 705
QY 111 TGGTCTCTCAATGAGATCTGCTGAGATCTGTGACATCTGTGAATGACA 170
Db 704 TGGTCTCTCAATGAGATCTGCTGAGATCTGTGACATCTGTGAATGACA 170
QY 171 AGAAGAACTTCACTGCTCATAGAGTGTGTGACAGATGACAGATCTGAGG 230
Db 644 ATCAAGGATATGATGATCAAAAGTCTGATGAGAGCTGACAGAGATGACA 595
QY 231 ATGATGAGATCTCAAAATGATCTCTGGTGAATCTATCAATGAGCTGACA 290
Db 984 ACTGATCTCAATCTTGAAGAGAGTCTACTGGGTGAATCTATGATGAGATGACA 525
QY 291 TGGTACAGAAATCTATCATGAAGAGAGCTCATGTTGGGAACCTTCTGTT 350
17-NOV-2000; 2000US-0249207
17-NOV-2000; 2000US-0249208
17-NOV-2000; 2000US-0249209
17-NOV-2000; 2000US-0249210
17-NOV-2000; 2000US-0249211
17-NOV-2000; 2000US-0249212
17-NOV-2000; 2000US-0249213
17-NOV-2000; 2000US-0249214
17-NOV-2000; 2000US-0249215
17-NOV-2000; 2000US-0249216
17-NOV-2000; 2000US-0249217
17-NOV-2000; 2000US-0249218
17-NOV-2000; 2000US-0249244
17-NOV-2000; 2000US-0249245
17-NOV-2000; 2000US-0249246
17-NOV-2000; 2000US-0249247
17-NOV-2000; 2000US-0249248
17-NOV-2000; 2000US-0249249
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01-DEC-2000; 2000US-0250298
01-DEC-2000; 2000US-0250391
05-DEC-2000; 2000US-0251030
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05-DEC-2000; 2000US-0251032
06-DEC-2000; 2000US-0251479
06-DEC-2000; 2000US-0251480
06-DEC-2000; 2000US-0251481
08-DEC-2000; 2000US-0251856
08-DEC-2000; 2000US-0251857
08-DEC-2000; 2000US-0251858
08-DEC-2000; 2000US-0251859
15-DEC-2000; 2000US-0251990
15-DEC-2000; 2000US-0251991
05-JAN-2001; 2001US-02519678
XX
XX (HUMAN) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition .
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XX Disclosure: SEQ ID NO 7972; 1287Pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX polypeptide having a reproductive system related antigens. These can be used
XX in the prevention, treatment or amelioration of reproductive system
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
XX
XX Sequence 4503 BP; 1360 A; 837 C; 792 G; 1514 T; 0 other;

QY 590 AAC-TTTAAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 648
DB 54073 ACCTTTTATATGCTAGCTGGACCAAAAAGGTT--ATTTTGAGATATGCTTTACTGT 54130
QY 649 ACTGATGCTGATGGAACACTACATATCTCTTGSTACACTGTA 693
DB 54131 GGTGGTCTGAAGCTGAATCTACATATCTCAGACAGAGTGTCCTGAA 54175
RESULT 14
ZD AAF212172 standard; DNA, 143068 BP.
AC AAF21272;
AC AAF21272;
AT 14-MAR-2001 (first entry)
DT 14-MAR-2001 (first entry)
DE Human low adenosine antisenase oligonucleotide related sequence #2839.
KW Low adenosine antisenase oligonucleotide; phosphorothioate; allergy;
KW human; ataxia disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory bronchiolitis; anti-inflammatory;
KW surfactant depletion; respiratory bronchiolitis; anti-inflammatory;
KW respiratory obstruction; pulmonary vasodilation; cystic fibrosis;
KW surfactant hypoduction; pulmonary vasodilation; ataxia; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW chronic obstructive pulmonary disease; lung transplantation rejection;
KW cancer; ss.
OS Homo sapiens.
PN M3020062736-A2.
PD 26-OCT-2000.
XX 24-MAR-2000, 2000MO-US08020.
PF PF
PR 06-APR-1999, 99US-0127958.
PA (UNEC)- UNIV EAST CAROLINA.
XX (UNEC)- UNIV EAST CAROLINA.
XX NY:SC JN;
PI NY:SC JN;
XX WPI: 2000-679539/66.
PT Low adenosine (A) content antisenase oligonucleotides which do not
PT trigger adenosine receptors during metabolism; useful e.g. for treating
PT cancers and respiratory obstructions -
PS Disclosure: Page 1186-1219; 1592pp; English.
CC The present invention describes low adenosine (A) content antisenase
CC oligonucleotides and compositions (1) comprising the low adenosine
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC It can have respiratory, bronchodilator, anti-inflammatory, analgesic,
CC immunomodulatory, and/or other biological and/or cytotoxic activities.
CC The antisenase oligonucleotides and (1) can be used to reduce the
CC expression and/or activity of target polypeptides associated with
CC respiratory disorders and malignancies, such as stimulating and
CC activating transcription factors, growth factors, cytokines, growth factors,
CC immunoglobulins and antibodies, antibody receptors, cytokine factors,
CC chemokines, endogenously produced specific and non-specific enzymes,
CC chemokine proteins, adhesion molecules and their receptors, cytokine
CC receptors, CNS (CNS) and peripheral nervous and non-nervous system, central
CC nervous system (CNS) and peripheral nervous and non-nervous system peptide
CC receptors, CNS (CNS) and peripheral nervous and non-nervous system peptide
CC receptors, growth factors, vasodilator peptides and non-peptide
CC receptors. Antisenase oligonucleotides may be used in this way to reduce
CC antisenase oligonucleotides may be used in this way to reduce
CC including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoduction which are associated with a disease or
CC condition. The antisenase oligonucleotides and compositions (1) can
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC asthma, and/or other respiratory disorders and malignancies, such as
CC and/or cancer. AAF21814 to AAF21543 represent human polynucleotide
CC fragments and antisenase oligonucleotides used in the exemplification of
CC the present invention.
XX Sequence 143068 BP; 41154 A: 30122 C: 32403 G: 39449 T: 0 other;
Query Match 39 28, Score 284.6, DB 21: Length 143068;
Best Local Similarity 71.61, prev. Max. 71.61, 143068, 143068, 143068;
Matches 475; Conservative 0; Mismatches 149; Indels 21; Gaps 7;
QY 57 TGTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 115
DB 53544 TGTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 53603
QY 116 TCTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 175
DB 53604 TCTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 53663
QY 176 GATTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 235
DB 53664 GATTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 53723
QY 236 TCTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 295
DB 53724 TCTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 53775
QY 296 CAGATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 355
DB 53776 TGTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 53835
QY 356 TTTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 415
DB 53836 TTTTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 53895
QY 416 GCTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 470
DB 53896 GCTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 53955
QY 471 GATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 530
DB 53956 GCTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 54012
QY 531 GGT-ATTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 589
DB 54013 ATGCTATTAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 54072
QY 580 AAC-TTTAAATGCTGGGATGAATATTCCTCTTATGATATGCTTTATTC 648
DB 54073 ACCTTTTATATGCTAGCTGGACCAAAAAGGTT--ATTTTGAGATATGCTTTACTGT 54130
QY 649 ACTGATGCTGATGGAACACTACATATCTCTTGSTACACTGTA 693
DB 54131 GGTGGTCTGAAGCTGAATCTACATATCTCAGACAGAGTGTCCTGAA 54175
RESULT 15
ZD AAF212172 standard; DNA, 143068 BP.
AC AAF21272;
AC AAF21272;
AT 14-MAR-2001 (first entry)
DT 28-JUL-2000 (first entry)
DE Human adenosine receptor related polynucleotide SEQ ID NO:2672.
XX human, adenosine receptor; low adenosine antisenase oligonucleotide;

GenCode version 3.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2003, 15:35:54 ; Search time 836.08 seconds
14547.434 Million cell updates/sec

Title: US-09-914-152-3_COPY_2000_2750

Perfect score: 751 c tctctctgggtcccaag.....tgatggagctggaagctcc 751

Sequence: 14547.434 Million cell updates/sec

Scoring table: INVERTED KW

Gap: 10.0, Gapext 1.0

Searched: 16134066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 2000000000

Maximum DB seq length: 2000000000

Post-processing: Minimum match 0%

Minimum match 10%

Deleting 1182.48 summaries

Database:

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40: em:estab.*

41: em:estab.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	309.2	41.2	515	14	BM61815	
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c	4	303.6	40.4	713	17	BM61815
c	5	301.2	40.1	318	10	BM61815
c	6	301	40.1	460	9	BM61815

7	297	39.5	857	17	BM61815	515 bp	mRNA	linear	EST 28-FEB-2002
8	290.6	38.7	914	9	BM61815	515 bp	mRNA	linear	EST 28-FEB-2002
c	9	290.4	38.7	480	14	BM701722	515 bp	mRNA	linear
c	11	289.8	38.6	512	9	BM189864	515 bp	mRNA	linear
c	13	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	14	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	15	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	16	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	17	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	18	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	19	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	20	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	21	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	22	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	23	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	24	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	25	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	26	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	27	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	28	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	29	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	30	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	31	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	32	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	33	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	34	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	35	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	36	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	37	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	38	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	39	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	40	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	41	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	42	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	43	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	44	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear
c	45	285.6	38.0	570	17	BM189864	515 bp	mRNA	linear

ALIGNMENTS

RESULT 1	BM61815	515 bp	mRNA	linear	EST 28-FEB-2002
LOCUS	US-09-914-152-3_COPY_2000_2750	515 bp	mRNA	linear	EST 28-FEB-2002
DEFINITION	US-09-914-152-3_COPY_2000_2750	515 bp	mRNA	linear	EST 28-FEB-2002
ACCESSION	BM61815	515 bp	mRNA	linear	EST 28-FEB-2002
VERSION	BM61815.1	515 bp	mRNA	linear	EST 28-FEB-2002
KEYWORDS	EST	515 bp	mRNA	linear	EST 28-FEB-2002
ORGANISM	Homo sapiens	515 bp	mRNA	linear	EST 28-FEB-2002
REFERENCE	BM61815	515 bp	mRNA	linear	EST 28-FEB-2002
AUTHORS	Bonaldi, F. Lemong, G. and Soares, M.B.	515 bp	mRNA	linear	EST 28-FEB-2002
TITLE	Normalization and subtraction: two approaches to facilitate gene	515 bp	mRNA	linear	EST 28-FEB-2002
JOURNAL	discovery	515 bp	mRNA	linear	EST 28-FEB-2002
MEDLINE	9704477	515 bp	mRNA	linear	EST 28-FEB-2002
COMMENT	Contact: Soares, MB	515 bp	mRNA	linear	EST 28-FEB-2002
	Program for Rat Gene Discovery and Mapping	515 bp	mRNA	linear	EST 28-FEB-2002
	431 Eastman Medical Research Building Iowa City, IA 52242, USA	515 bp	mRNA	linear	EST 28-FEB-2002
	Fax: 319 335 8350	515 bp	mRNA	linear	EST 28-FEB-2002
	Fax: 319 335 9565	515 bp	mRNA	linear	EST 28-FEB-2002
	Internet: soares@uiowa.edu	515 bp	mRNA	linear	EST 28-FEB-2002
	Tissue Procurement: Dr. Gregor	515 bp	mRNA	linear	EST 28-FEB-2002
	cDNA library preparation: Dr. M. Bento Soares, University of Iowa	515 bp	mRNA	linear	EST 28-FEB-2002
	cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa	515 bp	mRNA	linear	EST 28-FEB-2002
	cDNA sequencing by: Dr. M. Bento Soares, University of Iowa	515 bp	mRNA	linear	EST 28-FEB-2002

QY 405 TGATCTGAGGCGATCCGATTCAGCGAGACCTCCAGCAGTAAAGATTATGATCT 465
Db 115 CGATGTCAGCAGCATCACTCCAGCGAAGGCTCCAGCGAAGAGATGACCTCA 56
QY 456 CTAAAGCATCAGTAGACATTATGCACTTTTTCAGCAATNAGATTATTTTA 516
Db 55 CCGAAGGCTCAGATTGATATCAGCATTTTTTACGATNAGATTATTTTA 6

Search completed: April 11, 2003, 22:37:47
Job time : 844.08 secs

Genome version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.
On nucleic - nucleic search, using sw model
Run on: April 11, 2003, 15:37:18 : Search time 20.7377 seconds
(without alignments)
11106.080 Million cell updates/sec
Title: US-09-914-152-3_COPY_2000_2750
Perfect score: 751
Sequence: 1 cctgttgagctcccaaa.....tatggagcggaaatcc 751
Scoring table: IDENTITY_NUC
Gapop 10.0 : Gapext 1.0
Sequences: 441342 seqs, 15339381 residues
Total number of hits satisfying chosen parameters: 882724
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0A
Issued first 45 summaries
Database :
1: /cgn2_6/pdata1/ina/sb.comb.seq
2: /cgn2_6/pdata1/ina/sb.comb.seq
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5: /cgn2_6/pdata1/ina/sb.comb.seq
6: /cgn2_6/pdata1/ina/sb.comb.seq
Feed No. is the number of results predicted by chance to have a score, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	239.8	31.9	111112	4	US-09-711-150-3	
2	232.8	31.0	80346	4	US-09-078-294-3	
3	182.4	29.8	80955	4	US-09-078-294-3	
C	137.2	18.1	65043	4	US-09-821-736-3	
5	96.2	12.8	65933	4	US-09-105-424-11	
6	92.4	12.3	313	4	US-08-931-769A-234	
7	92.4	12.3	313	4	US-09-052-452-234	
8	92.4	12.3	313	4	US-09-052-452-234	
9	92.4	12.3	313	4	US-08-905-223-138	
C	10	90.4	12.0	329	4	US-08-931-769A-227
11	83.6	11.1	3046	4	US-08-931-769A-227	
12	83.6	11.1	3046	4	US-08-931-769A-227	
13	83.6	11.1	3046	4	US-08-931-769A-227	
14	60.8	8.1	4396	4	US-09-821-736-1	
C	15	54.2	7.2	1001	4	US-09-641-638-144
16	54.2	7.2	1001	4	US-09-641-638-144	
17	50.4	6.7	19557	5	PT-0582-0336-36	
18	47.8	6.4	21234	4	US-09-810-671-3	
19	46.7	6.3	5543	2	US-08-687-080-101	
20	46.7	6.3	5543	2	US-08-687-080-101	
21	46.4	6.2	1442	2	US-08-346-052C-120	
22	46.4	6.2	1442	2	US-08-450-673C-120	
C	23	46.4	6.2	19736	4	US-09-740-038-3
24	46.4	6.2	19736	4	US-09-740-038-3	
25	46.2	6.2	3609	4	US-09-705-150-1	
C	26	46.2	6.2	87350	3	US-08-781-891-79
C	27	46.2	6.2	87543	4	US-09-791-211-3

Sequence 1, Appli	US-08-247-946A-1	23	43.8	6.1	2336	1	US-08-247-946A-1	Sequence 1, Appli
Sequence 1, Appli	US-09-070-040-1	C 30	45.8	6.1	5359	2	US-09-070-040-1	Sequence 1, Appli
Sequence 1, Appli	US-09-357-746-1	C 31	45.8	6.1	5372	3	US-09-357-746-1	Sequence 1, Appli
Sequence 3, Appli	US-09-831-836-3	C 32	42.8	6.1	7000	4	US-09-831-836-3	Sequence 3, Appli
Sequence 13, Appli	US-08-320-314-13	C 34	45.4	6.0	654	1	US-08-320-314-13	Sequence 13, Appli
Sequence 1, Appli	US-08-708-107-1	C 35	45.4	6.0	694	1	US-08-708-107-1	Sequence 1, Appli
Sequence 528, App	US-09-385-92-528	C 37	45.2	6.0	915	2	US-09-385-92-528	Sequence 528, App
Sequence 3, Appli	US-03-488-856A-10	C 38	44.8	6.0	1394	4	US-03-488-856A-10	Sequence 3, Appli
Sequence 3, Appli	US-09-318-448-110	C 39	44.8	6.0	1856	4	US-09-318-448-110	Sequence 3, Appli
Sequence 3, Appli	US-09-797-906-3	C 41	44.6	5.9	8350	3	US-09-797-906-3	Sequence 3, Appli
Sequence 3, Appli	US-04-781-211-3	C 42	44.6	5.9	8753	4	US-04-781-211-3	Sequence 3, Appli
Sequence 1, Appli	US-09-022-461-1	C 43	44.4	5.9	1204	2	US-09-022-461-1	Sequence 1, Appli
Sequence 1, Appli	US-09-033-556-3	C 44	44.4	5.9	1204	2	US-09-033-556-3	Sequence 1, Appli
Sequence 7, Appli	US-09-208-932-7	C 45	44.4	5.9	7264	4	US-09-208-932-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
Sequence 741-150-3
Sequence 3, Application US/0941150
Patent No. 6436589
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS.
CURRENT APPLICATION NUMBER: US/09/741.150
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3 FastSeq for Windows Version 4.0
LENGTH: 112132
TYPE: DNA
Organism: Human
FEATURES
NAME/KEY: misc:feature
LOCATION: (1)...(112132)
QUALIFIER: ORGANIZATION: n = A, T, C or G
US-09-741-150-3

Query Match	31.9%	Score 239.8	DB 4	Length 112132
Matches	484	Conservative	162	Indels 57
Gaps	91			
QY	52	CACTTCATGATTAACCTTCAGTCAGAGAGTCCTCTTA-TGATCAACAAAG-AAG	109	
DB	42311	CAATTCATGATTAACCTTCAGAGAGTCCTCTTA-TGATCAACAAAGAAAG	43770	
QY	110	CGTTCCTTGAATGATCTACTCTGTCAGAGTCGTGACATTTGTGAATGATC	169	
DB	42371	CGGTCCTTGAATGATCTACTCTGTCAGAGTCGTGACATTTGTGAATGATC	42420	
QY	170	AAGAAACA	198	
DB	42431	AACCTTCATGTCAGCTTGTGAATCTCAACAGATTTGAATTCATCAACA	42490	
QY	199	TGTCATGATCA-GGATGACAGATTCAGAGAGTCATTCATTCATAAATGCTCT	257	
DB	42491	TAGTGTAAAGGACGACACAGAGGTTTGAAGAGTTCATTCATTCATAAATGCTCT	42550	
QY	258	TGTCGTGTAATTCCTTCATCAATCGGTCGTCATGACAGAGATTCATCATGAAAG	317	
DB	42551	ACGTGGGTAATTCCTTCATCAATCGGTCGTCATGACAGAGATTCATCATGAAAG	42610	
QY	318	AAGAGTCATTTGTCGCAATCTCATTTGTGTCATTTTGAAGAAATTCGCGACCA	377	

Db 1327 GTTG-----TTTAAAGAACTGGACAGCCCTAGCTTCAGAGCTGTGACCC-----1277
 QY 407 CAGTGAAGGCACTCCATATTGAGCGAGAACTCCGACGATCAAAAGATATGATCTC 466
 Db 1276 -----GATCACTCATATGAAGAAGCACTCCGACGAGAAAGATATGACATGAC 1224
 QY 467 TAAGAGCTAGTACGACATAGCATTTTAAAGCAATAGATTTTACGTAGATAT 526
 Db 1223 TGAATCTCAATGATGATGATGATTTTAAATTA-----AG 1169
 QY 527 GTATGTTTATTTAGGCAATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 586
 Db 1168 GTATGTTTATTTAGGCAATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 1109
 QY 587 CATAC--TTTAAATGATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 622
 Db 1108 CAATAC--TTTAAATGATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 1049
 QY 623 -CTCTTTATGATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 681
 Db 1048 CCACTCTTCAATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 989
 QY 682 GGTACACCTGTA 693
 Db 988 GGTATGCTGCTGTA 977

RESULT 4
 US-09-821-736-3/c
 : Sequence 3, Application US/09821736
 : Patent No. 6461843
 : GENERAL INFORMATION:
 : APPLICANT: MERKEL, Marion et al.
 : TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, AND USES
 : TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, AND USES
 : FILE REFERENCE: CL001216
 : CURRENT APPLICATION NUMBER: US/09/821.736
 : INVENTION PRIORITY DATE: 2001-03-30
 : NUMBER OF SEQ ID NOS: 5
 : SOFTWARE: FASTSEQ For Windows Version 4.0
 : SEQ ID NO 3
 : DESCRIPTION: 736
 : TYPE: DNA
 : ORGANISM: Human
 : FEATURE:
 : LOCATION: (1)...(736)
 : OTHER INFORMATION: n = A,T,C or G
 US-09-821-736-3

Query Match 25.1%: Score 188.6; DB 4; Length 14753.
 Best Local Similarity 71.8%: Pred. No. 2,6e-41;
 Matches 308; Conservative 0; Mismatches 104; Indels 17; Gaps 4;
 Db 64 AAACCTCTGATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 123
 Db 13031 ATAGTTTGCGGCAAGGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12972
 QY 123 ATGCAATTTGATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 182
 Db 12971 ATGCAATTTGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12912
 QY 183 CAGTGTTCATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 242
 Db 12911 CATCTCTCATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12853
 QY 243 TCAATTAATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 302
 Db 12852 TCAATTAATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12793
 QY 303 ATCTATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 358

Db 12792 ATCTCTCATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12793
 QY 359 TAAATTAATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 418
 Db 12732 TAAATTAATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12684
 QY 419 ATCTATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 478
 Db 12683 ATCTATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12624
 QY 479 TAAATTAATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 487
 Db 12623 TAAATTAATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 12615

RESULT 5
 US-09-784-316-3/c
 : Sequence 3, Application US/09784316
 : Patent No. 6461843
 : GENERAL INFORMATION:
 : APPLICANT: MERKEL, Marion et al.
 : TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, AND USES
 : TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, AND USES
 : FILE REFERENCE: CL001139
 : CURRENT APPLICATION NUMBER: US/09/784.316
 : INVENTION PRIORITY DATE: 2001-02-16
 : NUMBER OF SEQ ID NOS: 5
 : SOFTWARE: FASTSEQ For Windows Version 4.0
 : SEQ ID NOS: 316
 : LENGTH: 65042
 : TYPE: DNA
 : ORGANISM: Human
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (1)...(65042)
 : OTHER INFORMATION: n = A,T,C or G
 US-09-784-316-3

Query Match 18.3%: Score 137.2; DB 4; Length 65042.
 Best Local Similarity 70.2%: Pred. No. 3e-27;
 Matches 229; Conservative 0; Mismatches 98; Indels 9; Gaps 3;
 QY 373 GACACCCGACCTTCACACACACGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 432
 Db 19001 GACACCCGACCTTCACACACACGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 18942
 QY 432 GACACCCGACCTTCACACACACGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 492
 Db 18941 GACACCCGACCTTCACACACACGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 18882
 QY 493 TTTTAAATTAATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 552
 Db 18881 TTTTAAATTAATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 18823
 QY 552 ATATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 612
 Db 18762 ATATGATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 18763
 QY 613 AAGTATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 671
 Db 18763 AAGTATGATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 18710
 QY 672 TTTTAAATTAATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 697
 Db 18709 TTTTAAATTAATGATGATTTTAAAGCAATAGATTTTACGTAGATAT 18684

RESULT 6
 US-09-105-542A-11
 : Sequence 11, Application US/09105542A
 : Patent No. 6461843
 : GENERAL INFORMATION:
 : APPLICANT: MERKEL, Marion et al.
 : TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, AND USES
 : TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, AND USES
 : FILE REFERENCE: CL001139
 : CURRENT APPLICATION NUMBER: US/09/105.542A
 : INVENTION PRIORITY DATE: 2001-02-16
 : NUMBER OF SEQ ID NOS: 5
 : SOFTWARE: FASTSEQ For Windows Version 4.0
 : SEQ ID NOS: 542A
 : LENGTH: 65042
 : TYPE: DNA
 : ORGANISM: Human
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (1)...(65042)
 : OTHER INFORMATION: n = A,T,C or G
 US-09-105-542A-11

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1 APPLICANT: Bullerdick, Jörn
2 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES OF GENES OF THE
3 FILE REFERENCE NUMBER: US/09/091,789A
4 CURRENT APPLICATION NUMBER: US/09/105,142A
5 CURRENT FILING DATE: 1998-06-26
6 PRIOR FILING DATE: 1998-06-26
7 PRIOR FILING DATE: 1998-06-26
8 PRIOR FILING DATE: 1998-06-26
9 NUMBER OF SEQ ID NOS: 23
10 SOFTWARE: FASTSEQ for Windows version 4.0
11 TYPE: DNA
12 LENGTH: 533
13 ORGANISM: Homo sapiens
14 US-09-105-142A-11

15 Query Match
16 Best Local Similarity 12.8%; Score 96.2; DB 4; Length 533;
17 Matches 119; Conservative 0; Mismatches 28; Indels 5; Gaps 2;

18 QY 358 TTAAAGATGTGAGAGACACCCACCTTCAACACCATCAGCTGATGATGACGAGC 417
19 Db 251 TTAAAGATGTGAGAGACACCCACCTTCAACACCATCAGCTGATGATGACGAGC 310
20 QY 418 CATCCATCATGAGGAGGAGACCTC--CAGCAGTAAAGATATGATCTCTAAAGAT 474
21 Db 311 CATCCATCATGAGGAGGAGACCTC--CAGCAGTAAAGATATGATCTCTAAAGAT 370
22 QY 475 CAGTACAGCATCATGATTTTAAAGATTAAGTATTTTACGTAAAGTA 525
23 Db 371 CAGTACAGCATCATGATTTTAAAGATTAAGTATTTTACGTAAAGTA 419

24 RESULT 7
25 : Sequence 214, Application US/08991789A
26 : Patent No. 6225054
27 : GENES INFORMATION:
28 : APPLICANT: Prudakis, Tony N.
29 : APPLICANT: Read, Steven G.
30 : APPLICANT: Smith, John M.
31 : TITLE OF INVENTION: TREATMENT AND METHODS FOR THE
32 : NUMBER OF SEQUENCES: 292
33 : CORRESPONDENCE ADDRESS:
34 : STREET: 701 Fifth Avenue, Suite 6300
35 : CITY: Seattle
36 : STATE: Washington
37 : ZIP: 98104-7092
38 : COUNTRY: USA
39 : COMPUTER READABLE FORM:
40 : MEDIUM TYPE: Floppy disk
41 : OPERATING SYSTEM: PC-DOS/MS-DOS
42 : SOFTWARE: PatentIn Release #1.0, Version #1.30
43 : CURRENT APPLICATION DATA:
44 : FILING DATE: 11-Dec-1997
45 : CLASSIFICATION:
46 : ATTORNEY/AGENT INFORMATION:
47 : REGISTRATION NUMBER: 31392
48 : TELECOMMUNICATION INFORMATION:
49 : TELEPHONE: (206) 682-6030
50 : TELEFAX: (206) 682-6031
51 : INFORMATION FOR SEQ ID NO: 234:
52 : SEQUENCE CHARACTERISTICS:
53 : TYPE: nucleic acid
54 : STRANDEDNESS: single
55 : TOPOLOGY: linear
56 : ORIGINAL SOURCE: cDNA
57 : ORGANISM: Homo sapiens
58 : US-09-105-142A-11

59 Query Match
60 Best Local Similarity 12.8%; Score 92.4; DB 4; Length 313;
61 Matches 119; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

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1 : NUCLEIC TYPE: cDNA
2 : ORIGINAL SOURCE:
3 : ORGANISM: Homo sapiens
4 : SEQUENCE DESCRIPTION: SEQ ID NO: 234:
5 : US-09-991-789A-234
6 : Query Match
7 : Best Local Similarity 12.3%; Score 92.4; DB 4; Length 313;
8 : Matches 119; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
9 : QY 57 TCATGATAAAATTCATGATGATGAGAGCTGCTTTAT-GATGACAAAGAGGTGTT 115
10 Db 17 TCATGATAAAATTCATGATGATGAGAGCTGCTTTATGATGACAAAGAGGTGTT 115
11 QY 116 TCTTGAAATGGAATCTCTCTGCTGGAAGTCTGGAATGTTGTAATGACAGAAA 175
12 Db 77 TCTTGGAATGGAATCTCTCTGCTGGAAGTCTGGAATGTTGTAATGACAGAAA 136
13 QY 176 GAATTTACATGCTTCTACATGAGTTAG 301
14 Db 137 GAATTTACATGCTTCTACATGAGTTAG 162
15 : RESULT 8
16 : Sequence 214, Application US/09062431
17 : Patent No. 6344550
18 : GENES INFORMATION:
19 : APPLICANT: Prudakis, Tony N.
20 : APPLICANT: Smith, John M.
21 : APPLICANT: Read, Steven G.
22 : APPLICANT: Smith, John M.
23 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
24 : NUMBER OF SEQUENCES: 297
25 : CORRESPONDENCE ADDRESS:
26 : STREET: 6300 Columbia Center, 701 Fifth Avenue
27 : CITY: Seattle
28 : STATE: Washington
29 : ZIP: 98104-7092
30 : COUNTRY: USA
31 : COMPUTER READABLE FORM:
32 : MEDIUM TYPE: Floppy disk
33 : OPERATING SYSTEM: PC compatible
34 : SOFTWARE: PatentIn Release #1.0, Version #1.30
35 : CURRENT APPLICATION DATA:
36 : FILING DATE: 04-Apr-1997
37 : CLASSIFICATION:
38 : ATTORNEY/AGENT INFORMATION:
39 : REGISTRATION NUMBER: 31392
40 : TELECOMMUNICATION INFORMATION:
41 : TELEPHONE: (206) 682-6030
42 : TELEFAX: (206) 682-6031
43 : INFORMATION FOR SEQ ID NO: 234:
44 : SEQUENCE CHARACTERISTICS:
45 : TYPE: nucleic acid
46 : STRANDEDNESS: single
47 : TOPOLOGY: linear
48 : ORIGINAL SOURCE: cDNA
49 : ORGANISM: Homo sapiens
50 : US-09-062-451-234
51 : Query Match
52 : Best Local Similarity 12.3%; Score 92.4; DB 4; Length 313;
53 : Matches 119; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
54 : QY 57 TCATGATAAAATTCATGATGATGAGAGCTGCTTTAT-GATGACAAAGAGGTGTT 115

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? Patent No. 6225084
? GENERAL INFORMATION:
? APPLICANT: Frudakis, Tony N.
? APPLICANT: Smith, Steven G.
? REED: Steven G.
?
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
? TREATMENT AND DIAGNOSIS OF BREAST CANCER
?
? NUMBER OF SEQUENCES: 392
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Seed IP Law Group
? CITY: Seattle
? STATE: Washington
? COUNTRY: USA
? REGISTRATION NUMBER: 98104-7092
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA: US/06/991.789A
? FILING DATE: 04-APR-1997
? CLASSIFICATION: C4K00000
?
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 31,392
? REFERENCE/DOCKET NUMBER: 210121.41903
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 682-4900
? TELEFAX: (206) 682-4033
? INFORMATION FOR SEQ ID NO: 227:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 392 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 227:
US-08-91-789A-227
?
? Query Match 11.1% Score 83.6; DB 4; Length 3646;
? Matches 113; Conservative 0; Mismatches 49; Indels 0; Gaps 0:
?
? Oy 353 GTATTTAGAATTTGTCAGCAGACCCACCTTCACACACATGACCTGATCATGCA 412
? Db 3459 GAATTCGTCATGATCAGACGCGCTTACCTCTGAGCAGCAGCCGATGATCAGTCA 3518
? Oy 413 GAGGACATCATGATGAGCAGACCTTCGACAGTAAAGATTATGTTCTTAAAGG 472
? Db 3519 GCAAGCATCAGCAGACGACGCGCTTCACACGAAAGATTCTGATCATGATGAGA 3578
? Oy 473 ATGACATGATCATGATTTTAAAGTAAAGTATT 514
? Db 3579 CTTCGATGATCATGATTTTAAAGTAAAGTATT 3620
?
? RESULT 12
? Sequence 227, Application US/09062451
? Patent No. 6423456
? GENERAL INFORMATION:
? APPLICANT: Frudakis, Tony N.
? APPLICANT: Smith, Steven G.
? REED: Steven G.
?
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
? TREATMENT AND DIAGNOSIS OF BREAST CANCER
?
? NUMBER OF SEQUENCES: 247
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Seed IP Law Group
? CITY: Seattle
? STATE: Washington
? COUNTRY: USA
? REGISTRATION NUMBER: 98104-7092
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA: US/09/598.326
? FILING DATE: 20-Jun-2000
? CLASSIFICATION: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 33,332

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? COUNTRY: USA
? REGISTRATION NUMBER: 98104-7092
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA: US/09/962.451
? FILING DATE: 04-APR-1997
? CLASSIFICATION:
?
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 31,392
? REFERENCE/DOCKET NUMBER: 210121.41902
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 682-4900
? TELEFAX: (206) 682-4033
? INFORMATION FOR SEQ ID NO: 227:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 392 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 227:
US-09-062-451-227
?
? Query Match 11.1% Score 83.6; DB 4; Length 3646;
? Matches 113; Conservative 0; Mismatches 49; Indels 0; Gaps 0:
?
? Oy 353 GTATTTAGAATTTGTCAGCAGACCCACCTTCACACACATGACCTGATCATGCA 412
? Db 3459 GAATTCGTCATGATCAGACGCGCTTACCTCTGAGCAGCAGCCGATGATCAGTCA 3518
? Oy 413 GAGGACATCATGATGAGCAGACCTTCGACAGTAAAGATTATGTTCTTAAAGG 472
? Db 3519 GCAAGCATCAGCAGACGACGCGCTTCACACGAAAGATTCTGATCATGATGAGA 3578
? Oy 473 ATGACATGATCATGATTTTAAAGTAAAGTATT 514
? Db 3579 CTTCGATGATCATGATTTTAAAGTAAAGTATT 3620
?
? RESULT 13
? Sequence 227, Application US/09598326
? Patent No. 6423456
? GENERAL INFORMATION:
? APPLICANT: Frudakis, Tony N.
? APPLICANT: Smith, Steven G.
? REED: Steven G.
?
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
? TREATMENT AND DIAGNOSIS OF BREAST CANCER
?
? NUMBER OF SEQUENCES: 247
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Seed IP Law Group
? CITY: Seattle
? STATE: Washington
? COUNTRY: USA
? REGISTRATION NUMBER: 98104-7092
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA: US/09/598.326
? FILING DATE: 20-Jun-2000
? CLASSIFICATION: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 33,332

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US-09-954-456-1096

Query Match 40 14; Score 301; DB 10; Length 160;

Matches 371; Similarity 43%; Mismatches 80; Indels 2; Gaps 2;

Oy 65 AACCTCTGATGAGAGCTGCTCTAT-GATGACAAAGAGAGGGTTCGTGA 123
 Db 460 AACCTCTGATGAGAGAGGTGCTCTATGAGAGAGAGAGAGAGAGTGA 401
 Oy 124 TGGATCTCTGCTGATGAGAGCTGCTGACAACTGTGAAATGACAGAGAGTTAC 183
 Db 400 TGGATCTCTGATGAGAGCTGCTGACAACTGTGAAATGACAGAGAGTTAC 341
 Oy 184 ACTCTTCACTAGAGTACTTGTGATGAGAGAGAGAGATGAGAGATGAGATTC 341
 Db 340 AATATATCAATAGTACTTGTGATGAGAGAGAGAGAGAGAGTGTGAGAGATG 281
 Oy 244 TCAATATATCTCTCTGAGTATCAATGAGAGAGAGAGAGAGAGAGAGAGAA 303
 Db 280 TTGAAGAGAGCTTACTGTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAA 221
 Oy 304 TCTCTGATGAG 363
 Db 220 TCTTGTGAG 161
 Oy 364 AATCTGATGAG 403
 Db 160 AATCTGATGAG 103
 Oy 424 GATGAG 483
 Db 100 CTCGAG 41
 Oy 484 ATTAGCATTTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
 Db 40 ATCAGCATTTTTT-AGCATTAAGTATTTTA 9

RESULT 4

US-09-967-768A-316
 : Sequence 316; Application US/0967768A
 : Reference 316; Application US/0967768A
 : General Information:
 : APPLICANT: Augustus, Meera
 : TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat
 : FILE REFERENCE: 689290-72
 : CURRENT APPLICATION NUMBER: US/09/967,768A
 : PRIOR APPLICATION NUMBER: US/99/236,109
 : PRIOR FILING DATE: 2000-09-28
 : PRIOR APPLICATION NUMBER: US/60/236,034
 : PRIOR FILING DATE: 2000-09-28
 : PRIOR APPLICATION NUMBER: US/60/236,111
 : PRIOR FILING DATE: 2000-09-28
 : NUMBER OF SEQ ID NOS: 325
 : SOFTWARE: FASTSEQ for Windows Version 3.0
 : SEQ ID NO 316
 : LENGTH: 143068
 : ORGAN: DNA
 : ORGANISM: Homo sapiens
 : OTHER INFORMATION: n = A.T.C or G

US-09-967-768A-316

Query Match 39 24; Score 284.6; DB 10; Length 143068;

Best Match Similarity 71.44; Pseq No 54e-59; Length 143068;

Matches 477; Conservative 149; Mismatches 19; Indels 21; Gaps 7;

Oy 57 TCAATATCAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 115
 Db 5354 TCAATATCAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 53603
 Oy 116 TCTGATATGAGATCTACTCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 175

Db 53604 TCTGATATGAGATCTACTCTCTGATGAGAGAGAGAGAGAGAGAGAGAG 53663
 Oy 176 GATTTACAGAGTGTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235
 Db 53664 CATTGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 53723
 Oy 236 TTTCAATTTCAAAATAGTCTCTGTTGGGTAAATGCTTCAAAATGGCGTGGCA 295
 Db 53724 CTTGCTCTTCAAAATAGTCTCTGTTGGGTAAATGCTTCAAAATGGCGTGGCA 33775
 Oy 296 CAGAGATCAATCTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 355
 Db 53776 TGAAGATCAATCTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 53835
 Oy 356 TTTTACAAATTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
 Db 53836 TTTTACAAATTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 53895
 Oy 416 GCATCTCATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 53955
 Db 53896 GCATCTCATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 54012
 Oy 470 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
 Db 53956 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 54072
 Oy 531 GTT-ATTTTATGAGCATGCTCTATTTTATGAGCATTAAGTATTTTATGATGAT 589
 Db 54023 ATGCTGTTCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT 648
 Oy 590 AAC-TTTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 54072
 Db 54073 AAC-TTTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 54130
 Oy 649 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 693
 Db 54131 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 54175

RESULT 5

US-09-742-312-3/C
 : Sequence 3; Application US/09742312
 : Reference 3; Application US/09742312
 : General Information:
 : APPLICANT: CHANDROMOLISARAN, Ishwar et al
 : TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
 : TITLE OF INVENTION: NICOTIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.
 : FILE REFERENCE: CLO00838
 : CURRENT APPLICATION NUMBER: US/09/742,312
 : CURRENT FILING DATE: 2000-12-22
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 3
 : LENGTH: 471309
 : TYPE: CDS
 : ORGANISM: Human
 : FEATURE:
 : ANALYST: misc_feature
 : LOCKED: 1 (yes)
 : OTHER INFORMATION: n = A.T.C or G

US-09-742-312-3

Query Match 37 48; Score 280.6; DB 10; Length 147309;

Best Match Similarity 71.44; Pseq No 54e-59; Length 147309;

Matches 477; Conservative 162; Indels 29; Gaps 7;

Oy 52 GAGCTCTGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGAT 110
 Db 103595 CAATTTGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGAT 103536
 Oy 111 TGGTCTTCTGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGAT 170


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RESULT 7
? Sequence 7, Application US/09867701
? Patent No. US2002012237A1
? APPLICANT: Jones, Paul A.
? APPLICANT: Harlicker, Susan L.
? APPLICANT: Jones, Robert
? APPLICANT: Agajane, Paul A.
? TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
? FILE REFERENCE: 210121.497 US/09/867,701
? CURRENT FILING DATE: 2001-04-29
? CURRENT PILING DATE: 2001-04-29
? NUMBER OF SEQ ID NOS: 10912
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 5
? LENGTH: 10950
? TYPE: DNA
? ORGANISM: Homo sapien
? NAME/KEY: misc-feature
? LOCATION: (11)---(705)
? OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10950
Query Match 36.04; Score 270; DB 10; Length 705;
Best Local Similarity 70.64; Pred. No. 1-6e-57;
Matches 430; Conservative 0; Mismatches 165; Indels 14; Gaps 5;
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DB 687 GATGCAAGCAAGAGGTGGTCTTGAATGGAATCTACTCTGCTGAGAGTCTGTGAAC 155
OY 156 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
DB 627 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
OY 216 GCAAGTTCGAGAGGATCGATTCGATTCGAAATGAGTCTCTGTGGTAAATGCTTA 275
DB 627 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
OY 216 GCAAGTTCGAGAGGATCGATTCGATTCGAAATGAGTCTCTGTGGTAAATGCTTA 275
DB 627 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
OY 568 GCAAGTTCGAGAGGATCGATTCGATTCGAAATGAGTCTCTGTGGTAAATGCTTA 275
DB 627 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
OY 276 TCAATGATGCTGCTGATGAGCAAGATCTATCATGAGAGAGAGTCAATGATGTGG 335
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DB 627 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
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OY 448 CAACTGATCTGCTGATGAGCAAGATCTATCATGAGAGAGAGTCAATGATGTGG 395
DB 627 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
OY 396 ATGACCTGATGATGAGCAAGATCTATCATGAGAGAGAGTCAATGATGTGG 455
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OY 389 ACCACTGATGATGAGCAAGATCTATCATGAGAGAGAGTCAATGATGTGG 455
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DB 627 ATTGTTGGAATGAGCAAGAGATTTGACAGTGTATCTGAGTGTGATGACGAGTA 215
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RESULT 8
? Sequence 8, Application US/09844653
? Patent No. US2003005347A1
? APPLICANT: Jones, Paul A.
? APPLICANT: Agajane, Paul A.
? APPLICANT: Harlicker, Susan L.
? APPLICANT: Jones, Robert
? APPLICANT: Agajane, Paul A.
? TITLE OF INVENTION: Detecting and Treating Eye Disease
? FILE REFERENCE: 210121.497 US/09/844,653
? CURRENT FILING DATE: 2001-04-29
? CURRENT PILING DATE: 2001-04-29
? NUMBER OF SEQ ID NOS: 173
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 5
? LENGTH: 402850
? TYPE: DNA
? ORGANISM: Homo sapiens
? NAME/KEY: misc-feature
? LOCATION: (46565)---(46565)
? OTHER INFORMATION: The n at this position can be a, c, t, or g.
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OY 171 TGTGTTCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 230
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DB 342693 CAACTGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 409
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RESULT 11
US-09/795-668-1
Sequence 1 application US/09795668
General INFORMATION
Applicant: Stefanoson, Reelin
APPLICANT: Steintorsdottir, Valgerdur
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA G
FILE REFERENCE: 2345 2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIORITY DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SEQUENCE LISTING INFORMATION
SEQ ID NO: 1 seqidseq for Windows Version 4.0
LENGTH: 153841
TYPE: DNA
FEATURES
FEATURE: Homo sapiens
NAME/KEY misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: seq or c
NAME/KEY misc_feature
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US-09/795-668-1

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QY 611 TAAAA-----GTATTTGCTCTTTATGATATTTGCTTTATATGACATCTGTAAT 661
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Search completed: April 12, 2003, 04:33:45
Job time : 2685 sec

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RESULT 15
US-09-764-869-1953/C
: Sequence 1953. Application US/09764869
: Patent No. US2002006152A1
: Owner: Genentech, Inc.
: APPLICANT: Ewen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC007
: PRIORITY NUMBER: US/09/764,869
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 2442
: SOURCE: Genentech, Inc. (Genentech Ver. 2.0)
: SEQ ID NO 1953
: LENGTH: 32176
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-764-869-1953

Query Match
Similarity 32.9% Score 247.2; DB 10; Length 32176;
Matches 460; Conservative 4; Pairs 56;
Matches 133; Indels 31; Gaps 9;

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QY 133 CTCTGCTGAGATGCTGGAGCATCTGTAATGATACAGAGAGAAATTTACATGCTTACA 192
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Db 14379 GTTCTGTGTGGCTTAAATGCTGATGATGATGATGATGATGATGATGATGATG 14120
QY 313 AAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 372
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Db 14319 AAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 342
QY 373 GATCACCACCACTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 4265
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Db 14264 AGTCACCCCACTGTCAGATGATGATGATGATGATGATGATGATGATGATGATG 432
QY 433 CAGACACTCTGACAGG--TAAAGAGATATGATCTTTAAGGATCATGATGATGATG 491
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QY 492 TTTTAAAGCAATAAGATATTTTAACTAGATGATGATTTATTTTAAAGCATATGC 551
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Db 14148 TTTTAAAGCAATAAGATATTTTAACTAGATGATGATTTATTTTAAAGCATATGC 14089
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Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DD 19282 TCCACCCCTGGTTCACCTCTAGACACACCTTCCTTCAGCAGCAGTCAGATGC 159341
OY 121 CAGCTCTTCAGCGGGCTCAGATGCACACACTTCCTTCACGAGGCCAGACGCC 180
DD 15942 CAGCTCTTCAGCGGGCTCAGATGCACACACTTCCTTCACGAGGCCAGACGCC 159401
OY 181 CTGAGAGCTCCAGGCTGAGCTGCTTCCTTCGTCGACACTTCCTTCGCTCATATGGG 240
DD 159402 CTGAGAGCTCCAGGCTGAGCTGCTTCCTTCGTCGACACTTCCTTCGCTCATATGGG 159461
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DD 159461 CTTGGGCTATGTCCTCTACCTCAGACTCTCTTCAGGTCAGAGATGATCTGA 159521
OY 301 ACTTAATCTTCAGACCCCTTCAGTCTTCAGCTCTTCAGCTCTTCAGCTCTTCAGT 360
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